



Qy	1	GAATTGGGAGCGCCGACAGAGAGAGCTGCTGAGCCATGGCTGAAGGGGAAATACCA	60
Db	1	GAATTGGGAGCGCCGACAGAGAGAGCTGCTGAGCCATGGCTGAAGGGGAAATACCA	60
Qy	61	CTTCTCAGCCCTGACCGAGAGATTTAACTGCGCTCAGGGAAATTAAGAAGACCCAAAC	120
Db	61	CTTCTCAGCCCTGACCGAGAGATTTAACTGCGCTCAGGGAAATTAAGAAGACCCAAAC	120
Qy	121	TCCTCTACTGTAGCAACGGGGGGCCACTTCTCTGAGGATCTCTCCGATGGCACATGGTATG	180
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Query Match 99.2%; Score 633.2; DB 9; Length 638;

### Query 1

Best Local Similarity 99.5%; Pred. No. 7, 9e-169; Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAATTCGGGAACCGCCACAGCAGCAGCTGCTGAGCCATGCTGAGGGGGAATACCA 60  
 Db 1 GAATTCGGGAACCGCCACAGCAGCAGCTGCTGAGCCATGCTGAGGGGGAATACCA 60

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QY 121 TCTCTACTGTAGCAAGGGGGCCACTTCTGAGGATTCCTTCGGATGCGACAGTGATG 180  
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QY 241 AGGTGTATATAAGAGTACCGAGCTGCGCAGTACTTGGCCATGACACAGCGGCTTT 300  
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QY 361 ATTACACACCTTATATATCAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 420  
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QY 421 AGATGGAGCTGCAACGGGCTCTAAACCTCACTATGCGCAGAAAGCAATCTGTTTC 480  
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QY 481 TCCCTCTGCGAGCTCTCTCTGATTAAGAGATCTGTTCTGCTGCTGCTGCTGCTGCT 540  
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QY 541 GTTTCAGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
 Db 541 GTTTCAGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600

QY 601 AACCCCGAGCCACAGAGGCTGATTTGTAAGCAACTT 638  
 Db 601 AACCCCGAGCCACAGAGGCTGATTTGTAAGCAACTT 638

RESULT 4  
 BC032697  
 LOCUS  
 DEFINITION Homo sapiens fibroblast growth factor 1 (acidic), mRNA (cDNA clone MGC:44867 IMAGE:5403677), complete cds.  
 ACCESSION BC032697  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1073)  
 AUTHORS Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy J.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J.J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S., Krzywinski M.I., Skalska U., Smalov D.E., Schnerch A., Schein J.E., Jones S.J. and Marra M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257  
 12477932  
 2 (bases 1 to 1073)  
 Direct Submission  
 Strausberg, R.  
 Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: http://mgc.nci.nih.gov  
 Contact: MGC help desk  
 Email: c9aphs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;  
 Web site: http://www.nisc.nih.gov/  
 Contact: nisc.mgc@nih.gov  
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 Series: IRAC Plate: 69 Row: d Column: 4  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 15055546.

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 /lab\_host="DH10B"  
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 157. .543  
 /note="FGF, Region: Fibroblast growth factor. Fibroblast growth factors are a family of proteins involved in growth and differentiation in a wide range of contexts. These growth factors cause dimerization of their tyrosine kinase receptors leading to intracellular signaling. There are currently four known tyrosine kinase receptors for fibroblast growth factors. These receptors can each bind several different members of this family. Members of this family have a beta trefoil structure"  
 /db\_xref="CDD:pfam00167"

misc\_feature  
 Query Match 94.3%; Score 601.4; DB 9; Length 1073;  
 Best Local Similarity 98.7%; Pred. No. 9e-160;  
 Matches 627; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

ORIGIN

QY 5 TCGGACCGCCGACAGAGAGAGCTGCTGAGCCATGCTGAGGGGAAATCACCACCTT 64  
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Db 57 TCTTGAAGCGCCCAAGAGAGAGCTGCTGAGCCATGCTGAGGGGAAATCACCACCTT 116  
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QY 65 CACAGCCCTGACGAGAGAGTATATCTGCTCCAGGGAATATACAGAGAGCCCAACTCTCT 124  
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Db 237 AAGGACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 296  
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Db 597 TGGAGAGTGCAGAGCGGCTCTTAAATCTACTATGGCCAGAGCAATCTTGTCTCTCC 655  
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QY 604 CCCCAGCCGACAGAGCTGAGATTTGAGCAACTT 638  
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Db 656 CCCCAGCCGACAGAGCTGAGATTTGAGCAACTT 690  
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RESULT 5  
HSHGFL 2259 bp mRNA linear PRI 12-SEP-1993  
LOCUS Human mRNA for human heparin-binding growth factor 1/ acidic  
DEFINITION fibroblast growth factor.  
ACCESSION X51943  
VERSION X51943.1 GI:32435  
KEYWORDS fibroblast growth factor; growth factor; heparin-binding growth factor.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 2259)  
AUTHORS Chiu, I.M., Wang, W.P., and Lehtoma, K.  
TITLE Alternative splicing generates two forms of mRNA coding for human heparin-binding growth factor 1  
JOURNAL Oncogene 5 (5), 755-762 (1990)  
MEDLINE 90265618  
PUBMED 1693186  
REFERENCE 2 (bases 1 to 2259)  
AUTHORS Chiu, I.M.  
TITLE Direct Submission  
JOURNAL Submitted (20-FEB-1990) Chiu I.-M., Dept of Internal Medicine, Davis Medical Research Centre, The Ohio State University, 480 West 9th Ave, Columbus OH 43210, USA  
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/clone="pHGF.1, 1.2, 1.3, 1.4 and 1.5"  
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Query Match 94.3%; Score 601.4; DB 9; Length 2259;  
Best Local Similarity 98.7%; Pred. No. 9.2e-160;  
Matches 627; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

QY 5 TCGGACCGCCGACAGAGAGAGCTGCTGAGCCATGCTGAGGGGAAATCACCACCTT 64  
||  
Db 1 TCTTGAAGCGCCCAAGAGAGAGCTGCTGAGCCATGCTGAGGGGAAATCACCACCTT 60  
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QY 65 CACAGCCCTGACGAGAGAGTATATCTGCTCCAGGGAATATACAGAGAGCCCAACTCTCT 124  
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Db 61 CACAGCCCTGACGAGAGAGTATATCTGCTCCAGGGAATATACAGAGAGCCCAACTCTCT 120  
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QY 125 CTACTGTAGCAACGAGGAGGAGCTCTTCCGAGATGCTTCCGAGATGCGACAGTGGATGGAC 184  
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QY 604 CCCCAGCCGACAGAGCTGAGATTTGAGCAACTT 638  
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RESULT 6  
108090  
LOCUS 108090 638 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 4 from Patent EP 0298723.  
ACCESSION 108090  
VERSION 108090.1 GI:589198  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 638)  
AUTHORS Fiddes, J.C., Abraham, J.A. and Protter, A.



TITLE Recombinant fibroblast growth factors  
JOURNAL Patent: EP 0298723-A1 4 11-JAN-1989;  
FEATURES Location/Qualifiers  
source 1..638  
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ORIGIN

Query Match 86.2%; Score 549.8; DB 6; Length 638;  
Best Local Similarity 98.5%; Pred. No. 4.2e-145;  
Matches 576; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 3 ATTGGGAGCGGGCCACAGCAGCAGCTGCTGAGCCATGCGTGAAGGGGAAATCACCACC 62  
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DB 595 TTTCAGGGGTCTCCTCCTGGTGTGA-CCCAAAATGTTCCCTTGA 638

RESULT 7

LOCUS 109138 638 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 3 from Patent WO 8900198.  
ACCESSION 109138  
VERSION 109138.1 GI:588154  
KEYWORDS .  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 638)  
AUTHORS Fiddes,J.C., Abraham,J.A. and Protter,A.  
JOURNAL Patent: WO 8900198-A 3 12-JAN-1989;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"

ORIGIN

Query Match 86.2%; Score 549.8; DB 6; Length 638;  
Best Local Similarity 98.5%; Pred. No. 4.2e-145;  
Matches 576; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 3 ATTGGGAGCGGGCCACAGCAGCAGCTGCTGAGCCATGCGTGAAGGGGAAATCACCACC 62  
DB 55 AGTCTTGAAGCGCCACACAGCAGCAGCTGCTGAGCCATGCGTGAAGGGGAAATCACCACC 114

QY 63 TTCACAGCCCTCGACGAGAGTTTAATCTGCTCGAGGAAATACAGAGAGCCCAAACTC 122  
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QY 363 TACACACCTATATATCCAGAGCAGTCGAGAGAAATTTGGTTTGGCTTCAAGAAG 422  
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DB 475 AATGGAGCTGCAAAACGGGTCTTAAACTCACTATGCGCAGAGCAATCTTGTTC 534  
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DB 535 CCCCTGCCAGTCTCTTGATTAAGAGATCTGTCTGGGTGTTCACCATCCAGAGAG 594  
QY 542 TTTCAGGGGTCTCCTCCTGGTGTGACCCCAAAATGTTCCCTTGA 586  
DB 595 TTTCAGGGGTCTCCTCCTGGTGTGA-CCCAAAATGTTCCCTTGA 638

RESULT 8

LOCUS BTGFAR 4005 bp mRNA linear MAM 18-NOV-1993  
DEFINITION Bovine mRNA for acidic fibroblast growth factor.  
ACCESSION X13221 S47526  
VERSION X13221.1 GI:347  
KEYWORDS fibroblast growth factor acidic; growth factor.

SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 4005)  
AUTHORS Halley,C., Courtois,Y. and Laurent,M.  
TITLE Nucleotide sequence of bovine acidic fibroblast growth factor cDNA  
JOURNAL Nucleic Acids Res. 16 (22), 10913 (1988)  
MEDLINE 89083506  
PUBMED 3205724  
REFERENCE 2  
AUTHORS Philippe,J.M., Renaud,F., Desset,S., Laurent,M., Mallet,J.,  
Courtois,Y. and Edwards,J.B.  
TITLE Cloning of two different 5' untranslated exons of bovine acidic  
fibroblast growth factor by the single strand ligation to  
single-stranded cDNA methodology  
JOURNAL Biochem. Biophys. Res. Commun. 188 (2), 843-850 (1992)  
MEDLINE 93075172  
PUBMED 1280126  
REFERENCE 3 (bases 1 to 4005)  
AUTHORS Halley,C.  
TITLE Direct Submission  
JOURNAL Submitted (12-OCT-1988) Halley C., Inserm U118, 29 Rue Wilhem  
75016, Paris, France  
COMMENT see M13439 for overlapping sequence.  
FEATURES Location/Qualifiers  
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CDS

/note="unnamed protein product; acidic fibroblast growth factor (AA 1 - 155)"  
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ORIGIN

Query Match 77.1%; Score 491.8; DB 4; Length 4005;  
Best Local Similarity 88.3%; Pred. No. 1.4e-128;  
Matches 557; Conservative 0; Mismatches 72; Indels 2; Gaps 2;

QY 9 GAACGGCCACAGCGAGCTGTGAGCCGCTGAGCGGGAATACACACCTTCA 68  
DB 888 GAAACGCCACACAGCGAGCTGTGAGCGGGAATACACACCTTCA 947  
QY 69 GCCCTGACGAGAGCTTTAATCTGCTCCAGGGAATACAGAGGCCAACTCTCTAC 128  
DB 948 GCCCTGACTGAGAGTTTAACTGCTCTAGGCAATACAGAGGCCAACTCTCTAC 1007  
QY 129 TGTAGCAACGGGGGCGACTTCTGAGGATCTTCCGATGGGACAGTGGATGGCAAG 188  
DB 1008 TGCAGCAACGGGGGCGACTTCTGAGGATCTTCCGATGGGACAGTGGATGGCAAG 1067  
QY 189 GACAGAGGACACAGCACTTCACTGCGAGCTCAGTGGGAAAGCGTGGGGAGGTGTAT 248  
DB 1068 GACAGAGGACACAGCACTTCACTGCGAGCTCAGTGGGAAAGCGTGGGGAGGTGTAT 1127  
QY 249 ATAAAGAGTACCGAGCTGCGGCACTTGGGCACTGAGACGCGGGCTTTTATCGGC 308  
DB 1128 ATAAAGAGTACCGAGCTGCGGCACTTGGGCACTGAGACGCGGGCTTTTATCGGC 1187  
QY 309 TCACAGACACCAATAGGAAGTGTGCTGCGAAAGGCTGAGAGAGCAACATTACAAC 368  
DB 1188 TCACAGACACCAATAGGAAGTGTGCTGCGAAAGGCTGAGAGAGCAACATTACAAC 1247  
QY 369 ACCTATATATCCAGAGCATGAGAGAGATGCTGCTGGGCACTGAGAGAGCAATGGG 428  
DB 1248 ACCTATATATCCAGAGCATGAGAGAGATGCTGCTGGGCACTGAGAGAGCAATGGG 1307  
QY 429 AGCTGCAACGGCGCTTCAAACTCACTATGCGCAAGAACTTGTGTTCTCCCGCTG 488  
DB 1308 AGCTGCAACGGCGCTTCAAACTCACTATGCGCAAGAACTTGTGTTCTCCCGCTG 1367  
QY 489 CAGTCTCTCTGATTAAGAGATCTGTTCTGGTGTGACACTCCAGAGAGATTGGA 547  
DB 1368 CAGTCTCTCTGATTAAGAGATCTGTTCTGGTGTGACACTCCAGAGAGATTGGA 1427  
QY 548 GGGGTCTCACTGCTGACCCCAAAATGTTCCCTGACCATTTGGCTGAGCCCTTAAACCCC 607  
DB 1428 GGGGTCTCACTGCTGACCCCAAAATGTTCCCTGACCATTTGGCTGAGCCCTTAAACCCC 1486  
QY 608 AGCCACAGAGCTGCAATTTGTAAGCACTT 638  
DB 1487 GGGCCACAGAGCTGCAATTTGTAAGCACTT 1517

RESULT 9  
AR380845  
LOCUS AR380845  
DEFINITION Sequence 1390 from patent US 6607879.  
ACCESSION AR380845  
VERSION AR380845.1 GI:40088479  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 490)  
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.  
TITLE Compositions for the detection of blood cell and immunological response gene expression  
JOURNAL Patent: US 6607879-A 1390 19-AUG-2003;  
FEATURES Location/Qualifiers  
source 1..490  
/organism="unknown"

/mol\_type="genomic DNA"

ORIGIN

Query Match 76.1%; Score 485.2; DB 6; Length 490;  
Best Local Similarity 99.4%; Pred. No. 9.7e-127;  
Matches 487; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 29 CTGCTGAGCCATGCTGAAAGGGGAAATCACACCTTTCACAGCCCTGACCGAGAGTTTAA 88  
DB 1 CTGCTGAGCCATGCTGAAAGGGGAAATCACACCTTTCACAGCCCTGACCGAGAGTTTAA 60  
QY 89 TCTGCTCCAGGGAATACAGAGGCCAACTCTCTTCTTCTTCTGATGCAACGGGGGCACTT 148  
DB 61 TCTGCTCCAGGGAATACAGAGGCCAACTCTCTTCTTCTTCTGATGCAACGGGGGCACTT 120  
QY 149 CTGAGGATCTCTTCCGATGCGACAGTGGAGGACAGGAGGACAGGAGCCAGCACAT 208  
DB 121 CTGAGGATCTCTTCCGATGCGACAGTGGAGGACAGGAGGACAGGAGCCAGCACAT 180  
QY 209 TCAGCTGAGCTCAGTGGGAAAGCGTGGGGAGGTTGTATATAAGAGTACCGAGACTGG 268  
DB 181 TCAGCTGAGCTCAGTGGGAAAGCGTGGGGAGGTTGTATATAAGAGTACCGAGACTGG 240  
QY 269 CAGTACTTGGCCTGACACGACGCGGCTTTTATAGGCTCACAGACACCAATGAGGA 328  
DB 241 CAGTACTTGGCCTGACACGACGCGGCTTTTATAGGCTCACAGACACCAATGAGGA 300  
QY 329 ATGTTTGTCTGGAAGGCTGAGGAGAACATTAACAACCTATATATCAAGAGCA 388  
DB 301 ATGTTTGTCTGGAAGGCTGAGGAGAACATTAACAACCTATATATCAAGAGCA 360  
QY 389 TGCAGAGCAATTTGTTGCTGCGCTCAAGAGAAATGGGAGCTGCAACGGGCTCTAA 448  
DB 361 TGCAGAGCAATTTGTTGCTGCGCTCAAGAGAAATGGGAGCTGCAACGGGCTCTCG 420  
QY 449 AACTCCTATGCGCAGAAAGCAATTTGTTTCTCCCTGCGAGTCTCTTCTGATTAAG 508  
DB 421 GACTCCTATGCGCAGAAAGCAATTTGTTTCTCCCTGCGAGTCTCTTCTGATTAAG 480  
QY 509 AGATCTGTC 518  
DB 481 AGATCTGTC 490

RESULT 10  
HSAFGF  
LOCUS HSAFGF  
DEFINITION H.sapiens aFGF mRNA for acidic fibroblast growth factor.  
ACCESSION X65778  
VERSION X65778.1 GI:396163  
KEYWORDS fibroblast growth factor; fibroblast growth factor acidic.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 490)  
AUTHORS Yu,Y.L., Kha,H., Golden,J.A., Migchielsen,A.A., Goetzl,E.J. and Turck,C.W.  
TITLE An acidic fibroblast growth factor protein generated by alternate splicing acts like an antagonist  
JOURNAL J. Exp. Med. 175 (4), 1073-1080 (1992)

QY 509 AGATCTGTC 518  
DB 481 AGATCTGTC 490

QY 509 AGATCTGTC 518  
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QY 509 AGATCTGTC 518  
DB 481 AGATCTGTC 490

Query Match 74.3%; Score 474.2; DB 4; Length 668;  
 Best Local Similarity 88.3%; Pred. No. 1.3e-123;  
 Matches 538; Conservative 0; Mismatches 66; Indels 3; Gaps 2;

Qy 9 GAAGCCGCCAAGCAGCAGCTGCTGAGCCATGCTGAGGGGAAATCACACCTTCACA 68  
 Db 61 GAACAGCCCAACAAACAGCAGCTGCTGAGCCATGCTGAGGGGAAATCACACCTTCACG 120

Qy 69 GCGCTGACCGAGAGTTTATCTGCTCCAGGGAATACAGAGCCCAAACTTCCTCTAC 128  
 Db 121 GCGCTGACCGAGAGTTTATCTGCTCCAGGGAATACAGAGCCCAAACTTCCTCTAC 180

Qy 129 TGTGAGCAACGGGGGCGCACTTCTCTGAGGATCTTCCGATGGCACAGTGGATGGGAGCAAG 188  
 Db 181 TGTGAGCAACGGGGGCGCACTTCTCTGAGGATCTTCCGATGGCACAGTGGATGGGAGCAAG 240

Qy 189 GACGAGGAGCGACGACATTCAGCTGCAGCTCAGTSCGGAAGCGTGGGGAGGTGTAT 248  
 Db 241 GACGAGGAGCGACGACATTCAGCTGCAGCTCAGTSCGGAAGCGTGGGGAGGTGTAT 300

Qy 249 ATAAGAGTAGCAGAGCTGGCCCACTTGGCCATGGACACCGAGCGGCTTTTATACGGC 308  
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Qy 309 TCACAGACACCAATGAGGAATGTTCTGCTGGAAGGCTGAGAGGCTGAGAGACCATTACAC 368  
 Db 361 TCACAGACACCAATGAGGAATGTTCTGCTGGAAGGCTGAGAGGCTGAGAGACCATTACAC 420

Qy 369 ACCTATATATCCAGAGGATTCAGAGAGATTTGTTTGTGGCTCAAGAGGATGGG 428  
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Qy 429 AGCTCAAGAGGGGCTTAAATCTATGCGAGAGGATCTGTTCTTCTCCCTG 488  
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Qy 489 CAGTCTCTTCTGATTAAAGAGATCTGTTCTG--TGTGACCATCTCCAGAGAGTTTCG 546  
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Qy 547 AGGGGTCTCTACCTGTTGACCCCAAAATGTTCCCTTGACCATTTGGCTGGCTTAAGCC 606  
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Qy 607 CAGCCCAACA 615  
 Db 660 TGCCCAACA 668

RESULT 12  
 BTEGDF  
 LOCUS  
 DEFINITION Bovine mRNA for EDGF II (acidic eye-derived growth factor II).  
 ACCESSION X14032 S47526  
 VERSION X14032.1 GI:322  
 KEYWORDS acidic eye-derived growth factor II; growth factor.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 668)  
 AUTHORS Alterio, J., Halley, C., Brou, C., Soussi, T., Courtois, Y. and Laurent, M.  
 TITLE Characterization of a bovine acidic PGF cDNA clone and its expression in brain and retina  
 JOURNAL FEBS Lett. 242 (1), 41-46 (1988)  
 MEDLINE 89078619  
 PUBMED 2849564

REFERENCE 2  
 AUTHORS Philippe, J.M., Renaud, F., Desset, S., Laurent, M., Mallet, J., Courtois, Y. and Edwards, J.B.  
 TITLE Cloning of two different 5' untranslated exons of bovine acidic fibroblast growth factor by the single strand ligation to single-stranded cDNA methodology  
 JOURNAL Biochem. Biophys. Res. Commun. 188 (2), 843-850 (1992)  
 MEDLINE 93075172  
 PUBMED 1280126

FEATURES  
 Location/Qualifiers

Query Match 76.1%; Score 485.2; DB 9; Length 490;  
 Best Local Similarity 99.4%; Pred. No. 9.7e-127;  
 Matches 487; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 29 CTGCTGAGCCATGCTGAGGGGAAATCAACACCTTCAAGCCCTGACCGGAGAGTTTAA 88  
 Db 1 CTGCTGAGCCATGCTGAGGGGAAATCAACACCTTCAAGCCCTGACCGGAGAGTTTAA 60

Qy 89 TCTGCTTCAGGGAATTAACAAGCCCAAACTTCTCTACTGTAGCAAGGGGGCACTT 148  
 Db 61 TCTGCTTCAGGGAATTAACAAGCCCAAACTTCTCTACTGTAGCAAGGGGGCACTT 120

Qy 149 CTTGAGGATCTCTCCGATGGCACAGTGGATGGGACAAAGGACAGAGGACACAT 208  
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Qy 209 TCAGCTGCAGCTCAGTCCGGAAGCGTGGGGAGGTGTATTAAGAGTACCGAGCTGG 268  
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Qy 329 ATGTTTCTTGGGAAGCGTGGGGAGAACCAATACACACTATATATTCAGAGCA 388  
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Qy 389 TCAGAGAGAGATTTGTTTGTGGCTCAAGAGAGTGGGAGCTGCAACCGGCTCTTAA 448  
 Db 361 TCAGAGAGAGATTTGTTTGTGGCTCAAGAGAGTGGGAGCTGCAACCGGCTCTTAA 420

Qy 449 AACTCAGTATGCGGCAAGAGCAATCTGTTCTTCCCTGCGCAGTCTCTCTGATTAAG 508  
 Db 421 GACTCAGTATGCGGCAAGAGCAATCTGTTCTTCCCTGCGCAGTCTCTCTGATTAAG 480

Qy 509 AGATCTGTTC 518  
 Db 481 AGATCTGTTC 490

RESULT 11  
 BOVFGFAA  
 LOCUS Bovine acidic eye-derived fibroblast growth factor (EDGF II) mRNA, complete cds.  
 ACCESSION M35608.1 GI:163047  
 VERSION M35608.1  
 KEYWORDS acidic eye-derived fibroblast growth factor.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 668)  
 AUTHORS Alterio, J., Halley, C., Brou, C., Soussi, T., Courtois, Y. and Laurent, M.  
 TITLE Characterization of a bovine acidic PGF cDNA clone and its expression in brain and retina  
 JOURNAL FEBS Lett. 242 (1), 41-46 (1988)  
 MEDLINE 89078619  
 PUBMED 2849564

COMMENT Original source text: Bovine retina, cDNA to mRNA.  
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 /organism="Bos taurus"  
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CDS  
 Location/Qualifiers

ORIGIN

source 1..668 /organism="Bos taurus" /mol\_type="mRNA" /db\_xref="taxon:9913" /clone="11.32.12" /tissue\_type="retina" /clone\_lib="lambda gtl1" 51..558 /notes="unnamed protein product; acidic eye-derived growth factor II (AA 1 - 155)" /codon\_start=1 /protein\_id="CAA32192.1" /db\_xref="GI:323" /db\_xref="GOA:P03968" /db\_xref="SWISS-PROT:P03968" /translation="MARGETTFPAURKPNLPLGNKKPKLLVCSNGGYFLRLPDG TVDGTQRSDQHIQLQCAEBSIGVEYIKSTETGQFLAMDTDGLLYGSPINSECLFLE RLEENHYNTYISKHAEKHFVGLKNGKSKLGRTHFGKAILFLPLFVSSD"

CDS

Query Match 74.3%; Score 474.2; DB 4; Length 668; Best Local Similarity 88.3%; Pred. No. 1.3e-123; Matches 538; Conservative 0; Mismatches 68; Indels 3; Gaps 2;

QY 9 GAACGGCCACACGACGAGCTGTGAGCCATGCGTGAAGGGGAATCAACCTTCACA 58  
DB 61 GAACACGACCAACACGACGCTGCTGAGCCATGCGTGAAGGAGAAACACGACCTTCAG 120  
QY 69 GCGCTGACCGAGAGTTTAACTCTCTCCAGGGAATTTACAGAGGCCCAAACTCTCTAC 128  
DB 121 GCGCTGACCTGAGAGTTTAACTCTCTCTGAGCAATTAAGAGGCCCAAGCTCTCTAC 180  
QY 129 TGTAGCAAGGGGGCCACTTCTCTGAGGATCTTCCGATGCGGACAGTGGAGCAAGG 188  
DB 181 TGCAGCAAGGGGGGCTACTTCTCTGAGAACTCTCTCCAGATGGCAGTGGAGCAAG 240  
QY 189 GACAGAGCGCAGACACATTCAGCTGAGCTAGTGGGAAAGCGTGGGCGAGTGTAT 248  
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QY 249 ATAAAGAGTACCGAGCTGGCCAGTCTTGGCCATGACACCGAGCGGCTTTTATAGGG 308  
DB 301 ATTAAGAGTACCGAGCTGGCCAGTCTTGGCCATGACACCGAGCGGCTTTTATAGGG 360  
QY 309 TCACAGACACCAATAGGAGATTTCTCTGCGAAAGCTGGAGAGACCATTTACAC 368  
DB 361 TCACAGACACCAATAGGAGATTTCTCTGCGAAAGCTGGAGAGACCATTTACAC 420  
QY 369 ACCTATATCAAGAAGCATCAAGAGAAATGTTGTTTGGCTCTCAAGAAATGGG 428  
DB 421 ACCTATATCAAGAAGCATCAAGAGAAATGTTGTTTGGCTCTCAAGAAATGGG 480  
QY 429 AGCTGCAAGCGGCTCTAAACTCACTATGCGCAGAAAGCAATCTTGTCTCCCGCTG 488  
DB 481 AGCTGCAAGCGGCTCTAAACTCACTATGCGCAGAAAGCAATCTTGTCTCCCGCTG 540  
QY 489 CCAGTCTCTTGTGATTAAGAGATCTTGTCTG--TGTGACCACTCCAGAGAGTTGG 546  
DB 541 CCAGTCTCTTGTGATTAAGAGATCTTGTGTTGGTGGTGGTGGTGGTGGTGGTGG 600  
QY 547 AGGGGCTCTCACTGGTGTGACCCCAAAATGTTCTGACCATTTGGCTGGCTAAACCC 606  
DB 601 AGGGGCTCTCACTGGTGTGACCCCAAAATGTTCTGACCATTTGGCTGGCTAAACCC 659  
QY 607 CAGCCCA 615  
DB 660 TGGCCCA 668

RESULT 13 A49428 8501 bp DNA circular PAT 07-MAR-1997

LOCUS A49428

DEFINITION Sequence 1 from Patent WO9608572.

ACCESSION A49428

VERSION A49428.1 GI:2302907

KEYWORDS

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 8501) Cameron,B. and Crouzet,J. METHOD FOR THE PRODUCTION OF RECOMBINANT PROTEINS, PLASMIDS AND MODIFIED CELLS

JOURNAL Patent: WO 9608572-A 1 21-MAR-1996; RHONE-POULENC RORER SA (FR)

COMMENT Other publication AU 3475495 960329 Other publication FR 2724665 960322.

FEATURES Location/Qualifiers

source 1..8501 /organism="unidentified" /mol\_type="unassigned DNA" /db\_xref="taxon:32644"

ORIGIN

Query Match 73.8%; Score 470.6; DB 6; Length 8501; Best Local Similarity 99.2%; Pred. No. 1.5e-122; Matches 473; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 39 ATGCGTGAAGGGGAATCAACCTTCACAGCCCTGACGAGAGTGTATCTGCTCCA 98  
DB 108 ATGCGTGAAGGGGAATCAACCTTCACAGCCCTGACGAGAGTGTATCTGCTCCA 167  
QY 99 GCGAATTTACAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCCACTTCTCGAGGATC 158  
DB 168 GCGAATTTACAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCCACTTCTCGAGGATC 227  
QY 159 CTTCCGATGGCAGCATGTGATGGGCAAGGAGGAGGAGGAGCAGCAGCATTCAGCTGAG 218  
DB 228 CTTCCGATGGCAGCATGTGATGGGCAAGGAGGAGGAGGAGCAGCAGCATTCAGCTGAG 287  
QY 219 CTCAGTCGGAAGCGTGGGGGAGGTGTATATAAGAGTACCGAGCTGGCCAGTACTTG 278  
DB 288 CTCAGTCGGAAGCGTGGGGGAGGTGTATATAAGAGTACCGAGCTGGCCAGTACTTG 347  
QY 279 GCGATGGACACCGCGGGCTTTTATGCGCTCACAGACACCAATATGAGGAATGTTTCTC 338  
DB 348 GCGATGGACACCGCGGGCTTTTATGCGCTCACAGACACCAATATGAGGAATGTTTCTC 407  
QY 339 CTGGAAGGCTCGAGGAGCAACCATTAACACCTATATATCCAGAGAGCATGAGAGAG 398  
DB 408 CTGGAAGGCTCGAGGAGCAACCATTAACACCTATATATCCAGAGAGCATGAGAGAG 467  
QY 399 AATTGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAAGCGGCTCTCAAACTCACTAT 458  
DB 468 AATTGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAAGCGGCTCTCAAACTCACTAT 527  
QY 459 GCGCAGAGCAACTGTTGTTCTCCCGCTCGAGCTCTCTGATTAAAGAGATCTG 515  
DB 528 GCGCAGAGCAACTGTTGTTCTCCCGCTCGAGCTCTCTGATTAAAGAGATCTG 584

RESULT 14 108499 481 bp DNA linear PAT 02-DEC-1994

LOCUS 108499

DEFINITION Sequence 13 from Patent WO 8701728.

ACCESSION 108499

VERSION 108499.1 GI:588791

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 481) Fiddes,J.C. and Abraham,J.A. RECOMBINANT FIBROBLAST GROWTH FACTORS

JOURNAL Patent: WO 8701728-A 13 26-MAR-1987;

FEATURES Location/Qualifiers

source 1..481 /organism="unknown" /mol\_type="unassigned DNA"

ORIGIN

Query Match 72.7%; Score 464; DB 6; Length 481; Best Local Similarity 98.9%; Pred. No. 1e-120; Matches 467; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 37 CCATGGCTGAAGGGGAATCAACCTTCACAGCCCTGACGAGAGTGTATCTGCTC 96  
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QY 97 CAGGGAATTACAGAGCCCAAACTCTCTACTAGTACCAAGCGGGGCCACTTCTCGAGA 156  
Db 61 CAGGGAATTACAGAGCCCAAACTCTCTACTAGTACCAAGCGGGGCCACTTCTCGAGA 120  
QY 157 TCCTTCGGATGCGACAGTGGATCGGACAGAGGACGAGCAGCAGCATTCAGCTGC 216  
Db 121 TCCTTCGGATGCGACAGTGGATCGGACAGAGGACGAGCAGCAGCATTCAGCTGC 180  
QY 217 AGCTCAGTCCGGAAGAGGTTGGGAGAGGTGTATATAAGAGTACCGAGCTGGCCAGTCT 276  
Db 181 AGCTCAGTCCGGAAGAGGTTGGGAGAGGTGTATATAAGAGTACCGAGCTGGCCAGTCT 240  
QY 277 TGCCCATGAGACACCGCGGCTTTTATAGGCTCAGACACCAAAATGAGGAATGTTGT 336  
Db 241 TGCCCATGAGACACCGCGGCTTTTATAGGCTCAGACACCAAAATGAGGAATGTTGT 300  
QY 337 TCCTGGAAGGCTGGAGGAGAACATTAACACCTATATATCCAGAGCATGCAGAGA 396  
Db 301 TCCTGGAAGGCTGGAGGAGAACATTAACACCTATATATCCAGAGCATGCAGAGA 360  
QY 397 AGAATTGGTTTGTTCGCTCAAGAGGAATGGAGCTCCAAAGCGGTCTTAAACTCACT 456  
Db 361 AGAATTGGTTTGTTCGCTCAAGAGGAATGGAGCTCCAAAGCGGTCTTAAACTCACT 420  
QY 457 ATGGCCAGAAAGCAATCTTGTTCCTCCCTCGCAGTCTCTCTGTATTAAG 508  
Db 421 ATGGCCAGAAAGCAATCTTGTTCCTCCCTCGCAGTCTCTCTGTATTAAG 472

RESULT 15  
LOCUS 109297 481 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 10 from Patent WO 8902471.  
ACCESSION 109297  
VERSION 109297.1 GI:588003  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 481)  
AUTHORS Talma, K.D. and Hilliker, S.  
TITLE RECOMBINANT DNA CONSTRUCTS CONTAINING AN R3 PROMOTER  
JOURNAL Patent: WO 8902471-A 10 23-MAR-1989;  
FEATURES Location/Qualifiers  
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Query Match 72.7%; Score 464; DB 6; Length 481;  
Best Local Similarity 98.9%; Pred. No. 1e-120;  
Matches 467; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 37 CCATGGCTGAAGGGGAATCACCACCTTCCAGCGCTGACCGAGAGTTTAACTCGCTC 96  
Db 1 CCR1GGCTGAAGGGGAATCACCACCTTCCAGCGCTGACCGAGAGTTTAACTCGCTC 60  
QY 97 CAGGGAATTACAGAGCCCAAACTCTCTACTAGTACCAAGCGGGGCCACTTCTCGAGA 156  
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QY 157 TCCTTCGGATGCGACAGTGGATCGGACAGAGGACGAGCAGCAGCATTCAGCTGC 216  
Db 121 TCCTTCGGATGCGACAGTGGATCGGACAGAGGACGAGCAGCAGCATTCAGCTGC 180  
QY 217 AGCTCAGTCCGGAAGAGGTTGGGAGAGGTGTATATAAGAGTACCGAGCTGGCCAGTCT 276  
Db 181 AGCTCAGTCCGGAAGAGGTTGGGAGAGGTGTATATAAGAGTACCGAGCTGGCCAGTCT 240  
QY 277 TGCCCATGAGACACCGCGGCTTTTATAGGCTCAGACACCAAAATGAGGAATGTTGT 336  
Db 241 TGCCCATGAGACACCGCGGCTTTTATAGGCTCAGACACCAAAATGAGGAATGTTGT 300  
QY 337 TCCTGGAAGGCTGGAGGAGAACATTAACACCTATATATCCAGAGCATGCAGAGA 396  
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Db 361 AGAATTGGTTTGTTCGCTCAAGAGGAATGGAGCTCCAAAGCGGGTCTCTCGACTCACT 420  
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Db 421 ATGGCCAGAAAGCAATCTTGTTCCTCCCTCGCAGTCTCTCTGTATTAAG 472

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Maximum Match 100%  
Listing first 45 summaries

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8: Geneseq2003bs.\*  
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10: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	633.2	99.2	638	2	AA01723	Aax01723 Human end
6	633.2	99.2	638	8	ACF04028	Acf04028 Thrombin
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11	470.6	73.8	8501	2	AA712907	Aat12907 Novel exp
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14	463.2	72.6	468	6	ABV78179	Abv78179 Human DNA
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 XX 11-SEP-1987.  
 XX 02-MAR-1987; 87NO-US000425.  
 XX 03-MAR-1986; 86US-00835594.  
 XX (MELO-) MELOY LAB INC.  
 XX (RORE-) RORER BIOTECHNOLOGY INC.  
 XX Jaye M, Burgess W, Maciag T, Drohan W;  
 XX WPI; 1987-264128/37.  
 XX P-PSDB; AAP70482.  
 XX Human endothelial cell growth factor - produced by recombinant DNA techniques, useful for wound healing.  
 XX Example; Fig 8; 43pp; English.  
 XX To screen the human brain stem cDNA library for clones contg. ECGF inserts, a specific oligonucleotide was designed. This oligonucleotide was based upon a partial AA sequence analysis of the amino terminus of ECGF (see AAP70480 and AAP70481). Fig 3c sets forth for comparison the AA sequence of cyanogen bromide-cleaved bovine alpha and beta ECGF (AAP70834). The two clones that were isolated, ECGF clones 1 and 29, were analysed in further detail. The nucleotide sequence of these clones and the AA sequence deduced from the nucleic acid sequence is shown in Fig 8 (see AAP70788 and AAP70482). (Updated on 25-MAR-2003 to correct PF field.)  
 XX Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;  
 Query Match 99.2%; Score 633.2; DB 1; Length 638;  
 Best Local Similarity 99.5%; Pred. No. 3.5e-186;  
 Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GAATTCGGAGCGGCCACACGACGAGCTGCTGAGCCATGCTGGAAGGGGAATCACCA 60  
 DB 1 GAATTCGGAGCGGCCACACGACGAGCTGCTGAGCCATGCTGGAAGGGGAATCACCA 60  
 QY 61 CTTTCACAGCCTGACCGAGAGTTTAATCTGCTCCAGGGAAATTACAGAAGCCCAAC 120  
 DB 61 CTTTCACAGCCTGACCGAGAGTTTAATCTGCTCCAGGGAAATTACAGAAGCCCAAC 120  
 QY 121 TCCCTACTGTAGACGCGGGGCCCATCTTCGAGGATCTTCGGATGGACAGTGGATG 180  
 DB 121 TCCCTACTGTAGACGCGGGGCCCATCTTCGAGGATCTTCGGATGGACAGTGGATG 180  
 QY 181 GGACAGGACAGGAGCGACGACGACATTCAGCTGCGAGCTCAGTGGGAAAGCTGGGG 240  
 DB 181 GGACAGGACAGGAGCGACGACGACATTCAGCTGCGAGCTCAGTGGGAAAGCTGGGG 240  
 QY 241 AGGTGTATATAAGAGTACCGAGACTGGCCAGTCTTGGCCATGGACACCGAGGGCTTT 300  
 DB 241 AGGTGTATATAAGAGTACCGAGACTGGCCAGTCTTGGCCATGGACACCGAGGGCTTT 300  
 QY 301 TATAGGCTCACACACCAATAGGAATGTTGTTCTTGGAAAGCTGGAGGAAC 360  
 DB 301 TATAGGCTCACACACCAATAGGAATGTTGTTCTTGGAAAGCTGGAGGAAC 360  
 QY 361 ATTACACCTATATATCAAGAAGCATGCGAGAAATTTGTTGTCCTCAAGA 420  
 DB 361 ATTACACCTATATATCAAGAAGCATGCGAGAAATTTGTTGTCCTCAAGA 420  
 QY 421 AGAATGGAGCTGCAACGGGCTCTCGACTCTACTATGCGCCAGAAAGCAATCTTGTTTC 480

Db 421 AGAATGGAGCTGCAACGGGCTCTCGACTCTACTATGCGCCAGAAAGCAATCTTGTTTC 480  
 QY 481 TCCCTCGGAGCTCTCTGATTAAGAGATCTGTTCTGTTGTTGAGCACTCCAGAGAA 540  
 Db 481 TCCCTCGGAGCTCTCTGATTAAGAGATCTGTTCTGTTGTTGAGCACTCCAGAGAA 540  
 QY 541 GTTTCGAGGGTCTCTACCTGTTGACCCCAAAATGTTCCCTTGACCATTTGGCTGGCT 600  
 Db 541 GTTTCGAGGGTCTCTACCTGTTGACCCCAAAATGTTCCCTTGACCATTTGGCTGGCT 600  
 QY 601 AACCCCGCCAGAGAGCTGAATTTGTAAGCACTT 638  
 Db 601 AACCCCGCCAGAGAGCTGAATTTGTAAGCACTT 638  
 RESULT 3  
 AAT37503  
 ID AAT37503 standard; DNA; 638 BP.  
 XX AAT37503;  
 AC AAT37503;  
 XX 25-MAR-2003 (revised)  
 DT 29-DEC-1996 (first entry)  
 TT Human beta-endothelial cell growth factor.  
 DE Human beta-endothelial cell growth factor.  
 XX Endothelial cell growth factor; ECGF; blood vessel; regeneration;  
 KW heparin-Sepharose affinity chromatography; probe; oligonucleotide; FGF;  
 KM fibroblast growth factor; ss.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH CDS 39..506 /tag= a  
 FT misc\_RNA 42..503 /tag= b  
 FT /label= beta-ECGF  
 FT misc\_RNA 84..503 /tag= c  
 FT /label= acidic\_FGF  
 FT misc\_RNA 102..503 /tag= d  
 FT /label= alpha-ECGF  
 XX US5552528-A.  
 XX 03-SEP-1996.  
 XX 03-NOV-1994; 94US-00334884.  
 XX 03-MAR-1986; 86US-00835594.  
 PR 18-DEC-1987; 87US-00134499.  
 PR 29-APR-1991; 91US-00693079.  
 PR 27-NOV-1991; 91US-00799859.  
 XX (RHON) RHONE-POULENC RORER PHARM INC.  
 PA Maciag T, Burgess W;  
 FI WPI; 1996-412132/41.  
 XX P-PSDB; AAW04805, AAW04806, AAW04807.  
 DR Isolated, purified, biologically active bovine beta endothelial cell growth factor - useful to regenerate or treat damaged blood vessels.  
 XX Disclosure; Fig 8; 28pp; English.  
 CC Bovine beta-endothelial cell growth factor (beta-ECGF; AAW03999) having a mol.wt. of 20 kD can be purified at least 16300 fold from bovine brain using heparin-Sepharose affinity chromatography. ECGF is useful for among other purposes, diagnostic applications and has potential in the treatment of damaged blood vessels or other endothelial cell-lined structures. Human ECGF (AAT37503) or fragments may be obtained using oligonucleotides (AAT37504 and AAT37508 to AAT37509) whose design is based on the sequence of bovine alpha- and beta-ECGF. (Updated on 25-MAR-2003 to correct PF field.)  
 XX Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;

[illegible]



AC AAX01723;  
 DT 20-APR-1999 (first entry)  
 DE Human endothelial cell growth factor (ECGF) cDNA sequence.  
 KW Endothelial cell growth factor; ECGF; cleavable; recombinant; repair;  
 KW regenerate; blood vessel; endothelial cell; human; ss.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 39..506  
 FT /\*tag= a  
 FT /product= "ECGF"  
 FT misc\_feature 42  
 FT /\*tag= b  
 FT /note= "beta-ECGF begins at this position"  
 FT misc\_feature 84  
 FT /\*tag= c  
 FT /note= "acidic FGF begins at this position"  
 FT misc\_feature 102  
 FT /\*tag= d  
 FT /note= "alpha-ECGF begins at this position"  
 XX  
 XX US849538-A.  
 XX 15-DEC-1998.  
 XX 11-APR-1997; 97US-00840088.  
 XX 03-MAR-1986; 86US-00835594.  
 XX 18-DEC-1987; 87US-00134499.  
 XX 29-APR-1991; 91US-00693079.  
 XX 27-NOV-1991; 91US-00799859.  
 XX 03-NOV-1994; 94US-00334884.  
 XX 07-JUN-1995; 95US-00472964.  
 XX 04-NOV-1996; 96US-00743261.  
 XX (RHON ) RHONE-POULENC RORER PHARM INC.  
 XX  
 XX Jaye M, Burgess W, Maciag T, Drohan WN;  
 XX WPI; 1999-069734/06.  
 XX P-PSDB; AAW92291.  
 XX  
 XX DNA encoding a cleavable signal peptide and an endothelial cell growth  
 PT factor - useful for producing recombinant endothelial cell growth factor  
 PT proteins.  
 FT  
 XX Disclosure; Fig 8; 23pp; English.  
 XX  
 XX The invention relates to DNA encoding human endothelial cell growth  
 CC factors (ECGF) and plasmids comprising the DNA sequences. The DNA encodes  
 CC a cleavable signal peptide and an ECGF, where removal of the signal  
 CC peptide yields a mature form of the ECGF, where the ECGF is alpha-ECGF or  
 CC beta-ECGF. The DNA is used to produce recombinant ECGF proteins, which  
 CC can be used in treatments to repair or regenerate blood vessels or other  
 CC structures lined with endothelial cells. The present sequence represents  
 CC a human ECGF cDNA sequence (determined from lambda ECGF clones 1 and 29)  
 XX  
 XX Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;  
 SQ  
 Query Watch 99.2%; Score 633.2; DB 2; Length 638;  
 Best Local Similarity 99.5%; Pred. No. 3.5e-186;  
 Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GAATTGGGAAACCGCCAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAATCACC 60  
 DB 1 GAATTGGGAAACCGCCAGCAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAATCACC 60  
 QY 61 CTTTCACAGCCCTGACCGAGAGGTTTAATCTCTCCAGGGAATTACAGAGCCCAAC 120  
 DB 61 CTTTCACAGCCCTGACCGAGAGGTTTAATCTCTCCAGGGAATTACAGAGCCCAAC 120  
 QY 121 TCCCTCTACTGTAGCAACGGGGGCCATCTTCCTGAGGATCTTCCTGGATGCGATG 180  
 DB 121 TCCCTCTACTGTAGCAACGGGGGCCATCTTCCTGAGGATCTTCCTGGATGCGATG 180

QY 181 GGACAGGCGACAGAGCGACACACATTCAGCTGCGAGCTCAGTGGGAAGGCTGGGGG 240  
 DB 181 GGACAGGCGACAGAGCGACACACATTCAGCTGCGAGCTCAGTGGGAAGGCTGGGGG 240  
 QY 241 AGCTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGAGCGCTTT 300  
 DB 241 AGCTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGAGCGCTTT 300  
 QY 301 TATAGGCTCAGACAGACCAAAATGAGGAATGTTTCTTGGAAAGGCTGGAGGAGACC 360  
 DB 301 TATAGGCTCAGACAGACCAAAATGAGGAATGTTTCTTGGAAAGGCTGGAGGAGACC 360  
 QY 361 ATTACACACCTATATATCCAAAGAGCATGCAGAGAAGATTGGTTTGTGGCTCAAGA 420  
 DB 361 ATTACACACCTATATATCCAAAGAGCATGCAGAGAAGATTGGTTTGTGGCTCAAGA 420  
 QY 421 AGAATGGAGCTGCAAAAGCGGCTCTCGGACTCCTATGGCCAGAAAGCAATCTTTTTC 480  
 DB 421 AGAATGGAGCTGCAAAAGCGGCTCTCGGACTCCTATGGCCAGAAAGCAATCTTTTTC 480  
 QY 481 TCCCTCTCCAGTCTCTCTGATTAAAGAGATCTGTTCTGTGTTCGACCTCCAGAGAA 540  
 DB 481 TCCCTCTCCAGTCTCTCTGATTAAAGAGATCTGTTCTGTGTTCGACCTCCAGAGAA 540  
 QY 541 GTTTCGAGGCTCTCAGCTGGTGTGACCCCAAAATGTTCCCTGACCTGGCTGGCT 600  
 DB 541 GTTTCGAGGCTCTCAGCTGGTGTGACCCCAAAATGTTCCCTGACCTGGCTGGCT 600  
 QY 601 AACCCCGACGACAGAGCTGAAATTTGTAAGCACTT 638  
 DB 601 AACCCCGACGACAGAGCTGAAATTTGTAAGCACTT 638

RESULT 6  
 ACF04028  
 ID ACF04028 standard; DNA; 638 BP.  
 XX  
 AC ACF04028;  
 XX  
 DT 15-OCT-2003 (first entry)  
 XX  
 DE Thrombin resistant FGF-1 mutant production wildtype coding sequence.  
 XX  
 KW Thrombin resistant FGF-1; FGF-1; fibroblast growth factor-1;  
 KW myocardial ischaemia; peripheral vascular disease; cerebral ischaemia;  
 KW epithelial injury; epidermal wound injury; nerve injury; bone damage;  
 KW vasotropic; cardiant; cerebroprotective; vulnerary; neuroprotective;  
 KW osteopathic; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 42..506  
 FT /\*tag= a  
 FT /product= "FGF-1"  
 FT /partial  
 FT /note= "no start codon"  
 XX  
 PN WC2003052378-A2.  
 XX  
 XX 26-JUN-2003.  
 XX  
 XX 11-DEC-2002; 2002WO-US039686.  
 XX  
 XX 17-DEC-2001; 2001US-00022554.  
 XX  
 XX (REPA-) REPAIR INC.  
 XX (MAIN-) MAINE MEDICAL CENT RES INST.  
 XX  
 XX Maciag T, Ettenson DS, Burgess WH, Drohan WN;  
 XX WPI; 2003-559052/52.  
 XX P-PSDB; ABR63868.  
 XX  
 XX New thrombin degradation resistant fibroblast growth factor-1 (FGF-1)  
 PT polypeptide, useful for treating a disease or disorder, e.g. cerebral  
 PT ischemia or bone damage, or for enhancing the effectiveness of an FGF-1  
 PT response in a mammal.  
 XX

PS Claim 2; Fig 8; 83pp; English.

CC The present invention provides the protein and coding sequences of human  
CC fibroblast growth factor-1 (FGF-1) and a mutant that is resistant to  
CC thrombin degradation. The thrombin degradation resistant FGF-1 protein  
CC can be used for treating a disease or disorder (e.g. myocardial  
CC ischaemia, peripheral vascular disease, cerebral ischaemia, epithelial  
CC injury, epidermal wound injury, nerve injury, or bone damage), for  
CC enhancing the effectiveness of an FGF-1 response, or for stimulating an  
CC FGF-1 response in a mammal. The present sequence is the wildtype FGF-1  
CC coding sequence

XX SQ Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;

Query Match 99.2%; Score 633.2; DB 8; Length 638;  
Best Local Similarity 99.5%; Pred. No. 3.5e-186;  
Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAATTCGGAGAGCGCCACACAGCAGCAGCTGCTGAGCCATGGCTGAGGGGAATCACCA 60  
Db 1 GAATTCGGAGAGCGCCACACAGCAGCAGCTGCTGAGCCATGGCTGAGGGGAATCACCA 60  
Qy 61 CTTTCACAGCCCTGACGAGAGATTTAATCTGCTCCAGCGAATTACAGAGGCCCAAC 120  
Db 61 CTTTCACAGCCCTGACGAGAGATTTAATCTGCTCCAGCGAATTACAGAGGCCCAAC 120  
Qy 121 TCTCTACTGTAGCAAGGGGGCGACTTCTTCTGAGGATCTTCCGATGGGCACAGTGATG 180  
Db 121 TCTCTACTGTAGCAAGGGGGCGACTTCTTCTGAGGATCTTCCGATGGGCACAGTGATG 180  
Qy 181 GGACAAGGAGCAGGAGCGACACAGCATTTCAGCTCGAGCTCAGTCCGGAAGCGTGGGG 240  
Db 181 GGACAAGGAGCAGGAGCGACACAGCATTTCAGCTCGAGCTCAGTCCGGAAGCGTGGGG 240  
Qy 241 AGGTGTATTAAGAGTACCGAGCTGGCAGTCTTGGCCATGACACCGAGCGGCTTT 300  
Db 241 AGGTGTATTAAGAGTACCGAGCTGGCAGTCTTGGCCATGACACCGAGCGGCTTT 300  
Qy 301 TATACGGCTCACAGACCAATAGAGATTTTCTTCTGGAAAGGCTCGAGGAGAAC 360  
Db 301 TATACGGCTCACAGACCAATAGAGATTTTCTTCTGGAAAGGCTCGAGGAGAAC 360  
Qy 361 ATTACACACCTATATATCCAGAGCATGCGAGAGAAATTTGTTTGGCTCTAAGA 420  
Db 361 ATTACACACCTATATATCCAGAGCATGCGAGAGAAATTTGTTTGGCTCTAAGA 420  
Qy 421 AGAATGGAGCTGCMAAGCGGTCTCTAAACTCACTATGCCAAGAACTTTGTTTC 480  
Db 421 AGAATGGAGCTGCMAAGCGGTCTCTAAACTCACTATGCCAAGAACTTTGTTTC 480  
Qy 481 TCCCTCCGAGCTCTCTCTGATTAAGAGATCTGTTCTGGTGTGACACTCCAGAA 540  
Db 481 TCCCTCCGAGCTCTCTCTGATTAAGAGATCTGTTCTGGTGTGACACTCCAGAA 540  
Qy 541 GTTTCGAGGGCTCTCAGCTGGGTGACCCCAAAATGTTCCCTGACCATTTGGCTGGCT 600  
Db 541 GTTTCGAGGGCTCTCAGCTGGGTGACCCCAAAATGTTCCCTGACCATTTGGCTGGCT 600  
Qy 601 AACCCGAGCCCAAGAGCTGAAATTTGTAAGCACTT 638  
Db 601 AACCCGAGCCCAAGAGCTGAAATTTGTAAGCACTT 638

RESULT 7

AAT45985  
ID AAT45985 standard; cDNA; 639 BP.

XX AC AAT45985;

XX 25-MAR-2003 (revised)

DT 17-MAR-1997 (first entry)

XX Human endothelial cell growth factor cDNA.

XX Endothelial cell growth factor; EGF; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

CDS 1..507  
/\*tag= a

XX US5571790-A.

XX 05-NOV-1996.

XX 07-JUN-1995; 95US-00472964.

XX 03-MAR-1986; 86US-00835594.

XX 18-DEC-1987; 87US-00134499.

XX 29-APR-1991; 91US-00693079.

XX 27-NOV-1991; 91US-00799859.

XX 03-NOV-1994; 94US-00334884.

XX (RHON ) RHONE POULENC RORER PHARM INC.

XX Drohan WN, Jaye M, Maciag T, Burgess W;

XX WPI; 1996-505421/50.

XX P-PSDB; AAN06818.

XX Recombinant human endothelial cell growth factors - for treating damaged

XX blood vessels, etc.

XX Example D; Fig 8; 22pp; English.

XX A cDNA clone (AAT45985) codes for human endothelial cell growth factor  
XX (AAN06818). To obtain the clone, a human brain stem cDNA library was  
XX screened with a probe (see also AAT45986) based on N-terminal sequences  
XX of bovine EGF (see also AAN06819-20). EGF clones 1 and 29 were  
XX isolated, subcloned into M13mp8 and the EGF open reading frame and  
XX flanking regions sequenced by the chain termination method. DNA sequences  
XX (see also AAT45983-84) derived from the complete cDNA can be used in the  
XX large-scale prodn. of recombinant EGF beta (AAN06816) and alpha  
XX (AAN06817) in transformed host cells. (Updated on 25-MAR-2003 to correct  
XX PF field.)

XX SQ Sequence 639 BP; 172 A; 165 C; 168 G; 134 T; 0 U; 0 Other;

Query Match 97.5%; Score 622.2; DB 2; Length 639;

Best Local Similarity 99.4%; Pred. No. 9.3e-183;

Matches 635; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 1 GAATTCGGAGAGCGCCACACAGCAGCAGCTGCTGAGCCATGGCTGAGGGGAATCACCC 59  
Db 1 GAATTCGGAGAGCGCCACACAGCAGCAGCTGCTGAGCCATGGCTGAGGGGAATCACCC 60  
Qy 60 ACCTTCACAGCCCTGACGAGAGATTTAATCTGCTCCAGCGAATTACAGAGGCCCA 119  
Db 61 ACCTTCACAGCCCTGACGAGAGATTTAATCTGCTCCAGCGAATTACAGAGGCCCA 120  
Qy 120 CTCCTCTACTGTAGCAAGCGGGGCCACTTCTCTGAGGATCTTCCGATGGGCACAGTGAT 179  
Db 121 CTCCTCTACTGTAGCAAGCGGGGCCACTTCTCTGAGGATCTTCCGATGGGCACAGTGAT 180  
Qy 180 GGACAAGGAGCAGGAGCGACACAGCATTTCAGCTCGAGCTCAGTCCGGAAGCGTGGGG 239  
Db 181 GGACAAGGAGCAGGAGCGACACAGCATTTCAGCTCGAGCTCAGTCCGGAAGCGTGGGG 240  
Qy 240 GAGGTGTATTAAGAGTACCGAGACTGGCCAGTCTTGGCCATGACACCGAGCGGCTT 299  
Db 241 GAGGTGTATTAAGAGTACCGAGACTGGCCAGTCTTGGCCATGACACCGAGCGGCTT 300  
Qy 300 TTATACGGCTCACACACCAATAGAGATTTGTTTCTCGAAAGGCTCGAGGAGAAC 359  
Db 301 TTATACGGCTCACACACCAATAGAGATTTGTTTCTCGAAAGGCTCGAGGAGAAC 360  
Qy 360 CATTACACACCTATATATCCAGAGCATGCGAGAGAAATTTGTTTGGCTCTCAAG 419  
Db 361 CATTACACACCTATATATCCAGAGCATGCGAGAGAAATTTGTTTGGCTCTCAAG 420  
Qy 420 AGAATGGAGCTGCMAAGCGGTCTCTAAACTCACTATGCCAAGAACTTTGTTT 479  
Db 421 AGAATGGAGCTGCMAAGCGGTCTCTCTGATTAAGAGATCTGTTCTGGTGTGACCACTCCAGAA 480  
Qy 480 CTCCTCCGAGCTCTCTCTGATTAAGAGATCTGTTCTGGTGTGACCACTCCAGAA 539  
Db 481 CTCCTCCGAGCTCTCTCTGATTAAGAGATCTGTTCTGGTGTGACCACTCCAGAA 540

QY 540 AGTTTCGAGGGTCTCCTCAGCTGTGACCCAAATGTTCCCTTGACCAATGGCTGGCG 599  
|||||  
Db 541 AGTTTCGAGGGTCTCCTCAGCTGTGACCCAAATGTTCCCTTGACCAATGGCTGGCG 600  
|||||  
QY 600 TAAACCCCGAGCCAGAGAGCTGTAATTTGTAAGCAACTT 638  
|||||  
Db 601 TAAACCCCGAGCCAGAGAGCTGTAATTTGTAAGCAACTT 639  
|||||  
RESULT 8  
ACC42968  
ID ACC42968 standard; DNA; 2357 BP.  
XX  
AC ACC42968;  
XX  
XX 18-DEC-2003 (first entry)  
XX  
DE Human Fibroblast Growth Factor 1 coding sequence.  
XX  
KW Human; Fibroblast Growth Factor 1; FGF1; acidic FGF; aFGF;  
KW acidic Fibroblast Growth Factor; protein co-ordinate data; gene; ds.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 142..609  
FT /\*tag= a  
FT /product= "FGF1"  
XX  
XX W02003038054-A2.  
XX  
XX PD 08-MAY-2003.  
XX  
XX 31-OCT-2002; 2002MO-US034986.  
XX  
XX 31-OCT-2001; 2001US-0335583P.  
XX  
XX (UYNV ) UNIV NEW YORK STATE.  
XX  
XX Moosa M, Green DL, Linhard RV;  
XX  
XX WPI; 2003-482144/45.  
XX  
DR P-FSDB; ABR56165.  
XX  
XX Composition useful for identifying modulators of fibroblast growth factor  
FT -mediated signaling for use in treating cancer, has ternary complex of  
FT FGF-receptor, FGF ligand and heparin agonist or antagonist.  
XX  
XX Disclosure; Fig 165; 288pp; English.  
XX  
XX The present invention relates to an isolated composition comprising a  
CC ternary complex of an Fibroblast Growth Factor (FGF) ligand polypeptide  
CC (ABR56163, ABR56165), an FGF receptor polypeptide (ABR56164) and a  
CC heparin agonist or antagonist, where the agonist or antagonist binds to  
CC the FGF ligand polypeptide and the FGF receptor polypeptide to form the  
CC ternary complex. The composition is useful for identifying a compound  
CC that is an inhibitor of FGF receptor activity. FGF1 is also known as  
CC acidic FGF  
XX  
SQ Sequence 2357 BP; 691 A; 521 C; 567 G; 578 T; 0 U; 0 Other;

Db 286 ACAGGGGACAGGGGACCGACCAATTCAGCTGAGCTCAGTCCGGAAGGCTGGGGAG 345  
|||||  
QY 243 GTGTATATAAAGAGTACCGAGAGCTGGCCAGTCTTGGCCATGGACACCGAGGGCTTTTA 302  
|||||  
Db 346 GTGTATATAAAGAGTACCGAGAGCTGGCCAGTCTTGGCCATGGACACCGAGGGCTTTTA 405  
|||||  
QY 303 TACGGCTCACAGACACCAATAGGAATGTTTCTTCTGGAAGGCTGGAGAGAACCAT 362  
|||||  
Db 406 TACGGCTCACAGACACCAATAGGAATGTTTCTTCTGGAAGGCTGGAGAGAACCAT 465  
|||||  
QY 363 TACAACACTATATATCAAGAAGCATGACAGAGAGAAATGTTTGGCCCTCAAGAG 422  
|||||  
Db 466 TACAACACTATATATCAAGAAGCATGACAGAGAGAAATGTTTGGCCCTCAAGAG 525  
|||||  
QY 423 AATGGAGCTGCAAAACGGCTCTAAACTACTATGCCAGAAAGCAATCTGTTCTC 482  
|||||  
Db 526 AATGGAGCTGCAAAACGGCTCTCGACTACTATGCCAGAAAGCAATCTGTTCTC 585  
|||||  
QY 483 CCGCTGCGAGTCTCTCTCTGATTAAGAGATCTGTCT-GGTGTTCACACTCCAGAGAG 541  
|||||  
Db 586 CCGCTGCGAGTCTCTCTCTGATTAAGAGATCTGTCTGGGTGTTCACACTCCAGAGAG 645  
|||||  
QY 542 TTTCGAGGGTCTCTCAGCTGTGACCCAAATGTTCCCTTGACCAATGGCTGGCGTA 601  
|||||  
Db 646 TTTCGAGGGTCTCTCAGCTGTGACCCAAATGTTCCCTTGACCAATGGCTGGCGTA 704  
|||||  
QY 602 ACCCCAGCCACAGAGAGCTGTAATTTGTAAGCAACTT 638  
|||||  
Db 705 ACCCCAGCCACAGAGAGCTGTAATTTGTAAGCAACTT 741  
|||||  
RESULT 9  
ABX63225  
ID ABX63225 standard; cDNA; 4087 BP.  
XX  
AC ABX63225;  
XX  
XX 25-FEB-2003 (first entry)  
XX  
DE Human cDNA #225 differentially expressed in activated vascular tissue.  
XX  
KW Human; Gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant;  
KW hypotensive; antidiabetic; gynaecological; vasotropic; cerebroprotective;  
KW gene therapy; vascular disease; cancer; coronary; artery disease;  
KW hypertension; diabetes; pre-eclampsia; restenosis;  
KW ischaemia-reperfusion injury; stroke.  
XX  
XX Homo sapiens.  
XX  
XX US2002137081-A1.  
XX  
XX 26-SEP-2002.  
XX  
XX 08-JAN-2002; 2002US-00044090.  
XX  
XX 28-JUL-2000; 2000US-0222469P.  
XX  
XX 08-JAN-2001; 2001US-0260483P.  
XX  
XX (BAND/) BANDMAN O.  
XX  
XX Bandman O;  
XX  
XX WPI; 2003-110597/10.  
XX  
XX Combination for diagnosing, staging, treating, or monitoring the  
FT progression of treatment of a vascular disease, e.g. atherosclerosis,  
FT comprises several cDNAs that are differentially expressed in activated  
FT vascular tissue.  
XX  
XX Claim 1; Page; 18pp; English.  
XX  
XX This invention relates to a combination comprising several cDNAs that are  
CC differentially expressed in activated vascular tissue. The invention also  
CC discloses a high throughput method for detecting differentially expressed  
CC cDNAs in a sample. The cDNAs of the invention may have  
CC antiarteriosclerotic; cytostatic; cardiant; hypotensive; antidiabetic;  
CC gynaecological; vasotropic and cerebroprotective activities and may be  
CC used in gene therapy. The cDNAs of the invention may be used in a high-

CC throughput methods for detecting differential expression of one or more  
CC cDNAs in a sample, or screening several molecules or compounds to  
CC identify a molecule or compound that specifically binds a cDNA of the  
CC invention. A protein encoded by the cDNA may be used to screen several  
CC molecules or compounds to identify a ligand that specifically binds to  
CC the protein, or to produce or purify an antibody to the protein that can  
CC be used to detect a protein in a sample or purify a natural or  
CC recombinant protein from a sample. The nucleotides may be useful for  
CC diagnosing, staging, treating, or monitoring the progression of treatment  
CC of a vascular disease, e.g. atherosclerosis, cancer, coronary artery  
CC disease, hypertension, diabetes, pre-eclampsia, ischaemia- reperfusion  
CC injury, restenosis, or stroke. The cDNAs can also be used for large-scale  
CC genetic or gene expression analysis of several new nucleic acid  
CC molecules. Antibodies to the proteins encoded by the cDNAs are useful for  
CC diagnosing pre-pathologic disorders, and chronic or acute diseases  
CC associated with abnormalities in the expression, amount or distribution  
CC of the protein. The present sequence represents a cDNA of the invention  
CC that is differentially expressed in activated vascular tissue. Note: The  
CC sequence data for this patent did not form part of the specification, but  
CC was obtained in electronic format directly from USPTO at  
CC <http://seqdata.uspto.gov/sequence.html?DocID=20020137081>  
XX  
XX  
SQ Sequence 4087 BP; 1164 A; 886 C; 959 G; 1078 T; 0 U; 0 Other;

Query Match 94.3%; Score 601.8; DB 7; Length 4087;  
Best Local Similarity 98.6%; Pred. No. 4.9e-176;  
Matches 628; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 3 ATTGGGAGCGGCCACAGCAGCGCTGCTGAGCATGGCTGAAGGGGAATTCACACC 62  
Db 470 AGTCTTGAAGGCGCCACAGCAGCAGCTGTGAGCATGCTGAAGGGGAATTCACACC 529  
QY 63 TTCACGCGCTGACCGAGAGATTTAATCTGCTCCAGGGAAATTACAGAGCCCAATC 122  
Db 530 TTCACGCGCTGACCGAGAGATTTAATCTGCTCCAGGGAAATTACAGAGCCCAATC 589  
QY 123 CTCTACTGTAGCAACGGGGGCCACTTCTCCAGGATCTTCCGGATGGCAGTGGATGGG 182  
Db 590 CTCTACTGTAGCAACGGGGGCCACTTCTCCAGGATCTTCCGGATGGCAGTGGATGGG 649  
QY 183 ACAGGGACGAGGACGACAGCAGCATTCAGCTGCAGCTCAGTGCAGAGCGTGGGGAG 242  
Db 650 ACAGGGACGAGGACGACAGCAGCATTCAGCTGCAGCTCAGTGCAGAGCGTGGGGAG 709  
QY 243 GTGTATATAAGAGTACCGGAGCTGGCCAGTCTTGGCCATGGACCCGAGGGCTTTTA 302  
Db 710 GTGTATATAAGAGTACCGGAGCTGGCCAGTCTTGGCCATGGACCCGAGGGCTTTTA 769  
QY 303 TAGCGCTCAGACACCAATGAGGAATTTGTTCTCGGAAGCTGAGGAGAACCAT 362  
Db 770 TAGCGCTCAGACACCAATGAGGAATTTGTTCTCGGAAGCTGAGGAGAACCAT 829  
QY 363 TACACACCTTATATATCAAGAAGCATGCGAGAGAAATTGGTTTGTGGCTTCAAGAAG 422  
Db 830 TACACACCTTATATATCAAGAAGCATGCGAGAGAAATTGGTTTGTGGCTTCAAGAAG 889  
QY 423 AATGGAGCTGCAACCGGCTCTAAACTCAGTATGCGCAGGAAGCAATCTTGTTC 482  
Db 890 AATGGAGCTGCAACCGGCTCTCGAGCTCACTATGGCCAGGAAGCAATCTTGTTC 949  
QY 483 CCCCTGCCAGTCTCTCTGATTAAGAGATCTGTTCCT - GGTTGACCACTCAGAGAG 541  
Db 950 CCCCTGCCAGTCTCTCTGATTAAGAGATCTGTTCCTGAGTGTGACCACTCAGAGAG 1009  
QY 542 TTTCAGGGGCTCTCAGCTGGTGGACCCCAAAATGTTCCCTTGACCAATTTGGTGGCTA 601  
Db 1010 TTTCAGGGGCTCTCAGCTGGTGGAC - CCCAAAATGTTCCCTTGACCAATTTGGTGGCTA 1068  
QY 602 ACCCCAGGCCACAGAGCGCTGAAATTTGAGCACTT 638  
Db 1069 ACCCCAGGCCACAGAGCGCTGAAATTTGAGCACTT 1105

RESULT 10  
ID AAN93088  
ID AAN93088 standard; DNA; 638 BP.  
XX  
XX  
XX AAN93088;

DT 25-MAR-2003 (revised)  
DT 25-JUN-1990 (first entry)  
XX Acidic fibroblast growth factor.  
DE Acidic fibroblast growth factor.  
KW Acidic fibroblast growth factor; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FT mat\_peptide 91..555  
FT /\*tag= a  
XX /label= human acidic fibroblast growth factor  
XX EP298723-A.  
XX 11-JAN-1989.  
XX 06-JUL-1988; 88EP-00306158.  
XX 07-JUL-1987; 87US-00070797.  
XX (BIOU ) BIOTECH RES INST.  
XX Fiddes JC, Abraham JA, Protter A;  
XX WPI; 1989-009785/02.  
XX N-PSDB; AAN93087.  
XX Recombinant DNA encoding new fibroblast growth factor analogues - useful  
XX e.g. for accelerating wound healing and to control neovascularisation.  
XX Disclosure; Fig 2; 44pp; English.

CC The sequence encodes human acidic fibroblast growth factor (aFGF). See  
CC also AAN93087 and AAN93089. (Updated on 25-MAR-2003 to correct PA field.)  
XX  
XX Sequence 638 BP; 170 A; 156 C; 168 G; 144 T; 0 U; 0 Other;

Query Match 86.2%; Score 549.8; DB 1; Length 638;  
Best Local Similarity 98.5%; Pred. No. 3e-160;  
Matches 576; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 3 ATTGGGAGCGGCCACAGCAGCAGCTGCTGAGCATGGCTGAAGGGGAATTCACACC 62  
Db 55 AGTCTTGAAGGCGCCACAGCAGCAGCTGCTGAGCATGGCTGAAGGGGAATTCACACC 114  
QY 63 TTCACGCGCTGACCGAGAGATTTAATCTGCTCCAGGGAAATTACAGAGCCCAATC 122  
Db 115 TTCACGCGCTGACCGAGAGATTTAATCTGCTCCAGGGAAATTACAGAGCCCAATC 174  
QY 123 CTCTACTGTAGCAACGGGGGCCACTTCTCCAGGATCTTCCGGATGGCAGTGGATGGG 182  
Db 175 CTCTACTGTAGCAACGGGGGCCACTTCTCCAGGATCTTCCGGATGGCAGTGGATGGG 234  
QY 183 ACAGGGACGAGGACGACAGCAGCATTCAGCTGCAGCTCAGTGCAGGAAGCTGGGGAG 242  
Db 235 ACAGGGACGAGGACGACAGCAGCATTCAGCTGCAGCTCAGTGCAGGAAGCTGGGGAG 294  
QY 243 GTGTATATAAGAGTACCGGAGCTGGCCAGTCTTGGCCATGGACCCGAGGGCTTTTA 302  
Db 295 GTGTATATAAGAGTACCGGAGCTGGCCAGTCTTGGCCATGGACCCGAGGGCTTTTA 354  
QY 303 TAGCGCTCAGACACCAATGAGGAATTTGTTCTCGGAAGCTGAGGAGAACCAT 362  
Db 355 TAGCGCTCAGACACCAATGAGGAATTTGTTCTCGGAAGCTGAGGAGAACCAT 414  
QY 363 TACACACCTTATATATCAAGAAGCATGCGAGAGAAATTGGTTTGTGGCTTCAAGAAG 422  
Db 415 TACACACCTTATATATCAAGAAGCATGCGAGAGAAATTGGTTTGTGGCTTCAAGAAG 474  
QY 423 AATGGAGCTGCAACCGGCTCTAAACTCAGTATGCGCAGGAAGCAATCTTGTTC 482  
Db 475 AATGGAGCTGCAACCGGCTCTCGAGCTCACTATGGCCAGGAAGCAATCTTGTTC 534  
QY 483 CCCCTGCCAGTCTCTCTGATTAAGAGATCTGTTCCT - GGTTGACCACTCAGAGAG 541  
Db 535 CCCCTGCCAGTCTCTCTGATTAAGAGATCTGTTCCTGAGTGTGACCACTCAGAGAG 594

QY	219	CTCAGTCGGGAAAGCGCTGGGGGAGGTTGTATATAAAGAGTACCGAGACTGCCAGTACTTG	278
DB	288	CTCAGTCGGGAAAGCGCTGGGGGAGGTTGTATATAAAGAGTACCGAGACTGCCAGTACTTG	347
QY	279	GCCATCGGACACCGACACGGCGCTTTATACGGCTCACAACACCAAAATGAGGAATGTTTGTC	338
DB	348	GCCATCGGACACCGACACGGCGCTTTATACGGCTCACAACACCAAAATGAGGAATGTTTGTC	407
QY	339	CTGGAAAGGCTGGAGAGAGACCAATTACACACCTTATATATCCAGAGACATCGAGAGAG	398
DB	408	CTGGAAAGGCTGGAGAGAGACCAATTACACACCTTATATATCCAGAGACATCGAGAGAG	467
QY	399	AATGTGTTTGTGTGGCTTCAAGAGATGGGAGCTGCAAAACGGGTCCTAAAACCTCACTAT	458
DB	468	AATGTGTTTGTGTGGCTTCAAGAGATGGGAGCTGCAAAACGGGTCCTCGGACTCACTAT	527
QY	459	GGCCAGAAGCAATCTTGTTTCTCCCGCTGCCAGTCTCTTCTGATTAAGAGATCTG	515
DB	528	GGCCAGAAGCAATCTTGTTTCTCCCGCTGCCAGTCTCTTCTGATTAAGAGATCTG	584

RESULT 12  
AAN71029  
ID AAN71029 standard: DNA; 481 BP.

AA71029	AA71029 standard; DNA; 481 BP.
XX	
AC	AA71029;
XX	
XX	
DT	18-APR-1991 (first entry)
XX	
DE	Sequence of partially synthetic gene for human acidic fibroblast growth factor (FGF).
DE	
XX	
XX	
KW	Wound healing; tissue repair; tumour probe; ds.
XX	
XX	
OS	Homo sapiens.
XX	
PN	W08701728-A.
XX	
PD	26-MAR-1987.
XX	
PF	11-SEP-1986; 86WO-US001879.
XX	
XX	
PR	12-SEP-1985; 85US-00775521.
XX	
PR	16-DEC-1985; 85US-00809163.
XX	
PR	30-MAY-1986; 86US-00866932.
XX	

XX (BIOT-) BIOTECHN RES PARTNE.  
XX FPA  
XX  
XX Fiddes JC, Abraham JA;  
XX  
XX WPI; 1987-093786/13.  
XX  
XX New DNA sequences encoding mammalian fibroblast growth factors - useful  
XX in prodn. of pure factors for use in wound healing and tissue repair and  
XX of probe for tumour testing.  
XX  
XX Example; Fig 9; 89pp; English.  
XX  
XX The N-terminal AA sequence of both acidic and basic bovine FGF are used  
XX to construct long probes to screen human and bovine genomic libraries for  
XX FGF genes. Isolated sequences are used in vector construction etc. and  
XX used to transform CV-1 cells for FGF prodn

```

XX
SQ Sequence 481 BP; 133 A; 118 C; 129 G; 101 T; 0 U; 0 Other;
Query Match 72.7%; Score 464; DB 1; Length 481;
Best Local Similarity 98.9%; Pred. No. 1.2e-133;
Matches 467; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

[illegible]

Db 121 TCCTTCGGATGCGACAGTGGATGGGCAAGGCGACAGGCGACGACACATTCAGCTGC 180

QY 217 AGCTCAGTGGCGAAGACCTGGGGAGGTGTATATAAGAGTACCGAGCTGGCGAGTACT 276

Db 181 AGCTCAGTGGCGAAGACCTGGGGAGGTGTATATAAGAGTACCGAGCTGGCGAGTACT 240

QY 277 TGGCCATGCGACCGGCGCTTTTATACGGCTCCACAGCACCAAAATGAGGAATGTTTGT 336

Db 241 TGGCTATGCGACCGGCGCTTTTATACGGCTCCACAGCACCAAAATGAGGAATGTTTGT 300

QY 337 TCTGTGAAGGCTGGAGGAGGAGCCATACACACTATATATCCAGAGAGTCGACGAGA 396

Db 301 TCTGTGAAGGCTGGAGGAGGAGCCATACACACTATATATCCAGAGAGTCGACGAGA 360

QY 397 AGAATGTGTTTGTGTGGCTCAAGAGAGTGGAGCTGCAACCGCGTCTTAAAACTCACT 456

Db 361 AGAATGTGTTTGTGTGGCTCAAGAGAGTGGAGCTGCAACCGCGTCTTAAAACTCACT 420

QY 457 ATGGCCAGAAAGCAATCTTGTTCCTCCCTCCGAGTCTCTTCTGATTAAG 508

Db 421 ATGGCCAGAAAGCAATCTTGTTCCTCCCTCCGAGTCTCTTCTGATTAAG 472

RESULT 13

AA90994

ID AA90994 standard; DNA; 481 BP.

XX

AC AA90994;

XX

DT 25-MAR-2003 (revised)

DT 28-JUN-1990 (first entry)

XX

DE Partially synthetic nucleotide sequence encoding human acidic fibroblast growth factor (haFGF).

XX

KW Human acidic fibroblast growth factor; synthetic gene; lambda HAG-9.1;

KW PAL12-haFGF; PAL13-haFGF; E. coli r3 promoter.

XX

OS Homo sapiens.

XX

PH Key

FT Location/Qualifiers

FT misc\_feature

FT complement(1..122)

FT /tag= b

FT /notes= "As above"

FT 1..118

FT /tag= a

FT /notes= "from genomic lambda HAG-9.1 clone"

FT 3..5

FT /tag= w

FT /notes= "Believed to be the start codon for pro sequence of haFGF"

FT 119..154

FT /tag= c

FT /note= "oligo 1"

FT complement(123..158)

FT /tag= d

FT /note= "oligo 11"

FT 155..190

FT /tag= e

FT /note= "oligo 2"

FT complement(159..194)

FT /tag= f

FT /note= "oligo 12"

FT 191..226

FT /tag= g

FT /note= "oligo 3"

FT complement(195..230)

FT /tag= h

FT /note= "oligo 13"

FT 230..262

FT /tag= i

FT /note= "oligo 4"

FT complement(231..266)

FT /tag= j

FT /note= "oligo 14"

FT complement(245)

FT /tag= x

FT /note= "Differs from haFGF cDNA sequence of Jaye et al in

FT

FT mutation

FT which this base was G. "

245

FT /tag= x

FT /note= "Differs from haFGF cDNA sequence of Jaye et al in which this base was C. "

263..299

FT /tag= k

FT /note= "oligo 5"

FT complement(267..303)

FT /tag= l

FT /note= "oligo 15"

FT 300..334

FT /tag= m

FT /note= "oligo 6"

FT complement(304..338)

FT /tag= n

FT /note= "oligo 16"

FT 335..370

FT /tag= o

FT /note= "oligo 7"

FT complement(339..374)

FT /tag= p

FT /note= "oligo 17"

FT 371..406

FT /tag= q

FT /note= "oligo 8"

FT complement(375..410)

FT /tag= r

FT /note= "oligo 18"

FT 407..442

FT /tag= s

FT /note= "oligo 9"

FT complement(411..446)

FT /tag= t

FT /note= "oligo 19"

FT 443..476

FT /tag= u

FT /note= "oligo 10"

FT complement(447..480)

FT /tag= v

FT /note= "oligo 20"

FT

XX WO8902471-A.

PN

XX 23-MAR-1989.

PD

XX

PF 02-SEP-1988; 88WO-US003080.

XX

PR 11-SEP-1987; 87US-00095742.

XX

PA (CALD ) CALIFORNIA BIOTECHNOLOGY INC.

XX

PI Talmadge KD, Hilliker S;

XX

PI MPI; 1989-100011/13.

XX

DR DNA constructs contg. R3 promoter from E. coli - having high strength and being insensitive to catabolite repression.

XX

PS Fig 10; Page 7; 70pp; English.

XX

CC This sequence is referred to in the spec. as both Figure 10 and Figure 11. The 5' portion of the gene was provided by genomic lambda HAG-9.1 clone. This portion encodes the 15 amino acids of the pro sequence along with the first 25 amino acids of the mature 'primary' form of haFGF. The remainder was constructed from synthetic oligo- nucleotides designed so as to yield the same nucleotide sequence as that reported for haFGF cDNA by Jaye et al with 2 exceptions. One (see FT) was designed to destroy the NcoI site spanning codon 67 and the other was designed so as to add HindIII and EcoRI cleavage sites following the TGA termination codon. Neither of these changes affects the amino acid sequence encoded. The synthetic gene is inserted into pAL12 and pAL13 making pAL12-haFGF and pAL13-haFGF respectively. It is part of a construct comprising a first nucleotide sequence comprising an E. coli r3 promoter operably linked to a transcription initiation sequence; a second nucleotide sequence to terminate transcription; a third sequence comprising a ribosomal binding site and translation initiation codon operably linked to r3; a fourth sequence encoding a heterologous structural gene (eg AAN90994); a fifth sequence of an A-T rich oligomer; and a sixth sequence which is an

CC operator sequence to regulate expression of the fourth sequence. (Updated  
CC on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 481 BP; 133 A; 118 C; 129 G; 101 T; 0 U; 0 Other;  
Query Match 72.7%; Score 464; DB 1; Length 481;  
Best Local Similarity 98.9%; Pred. No. 1.2e-133;  
Matches 467; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 37 CCATGGCTGAAGGGGAATCACCACCTTCACAGCCCTGACCGAGAGTTTAACTGCTC 96  
DB 1 CCATGGCTGAAGGGGAATCACCACCTTCACAGCCCTGACCGAGAGTTTAACTGCTC 60  
QY 97 CAGGGAATTACAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCACTTCTCTAGGA 156  
DB 61 CAGGGAATTACAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCACTTCTCTAGGA 120  
QY 157 TCTTTCGGATGCGACAGTGGATGGGACAGGCGACAGGCGACACGACATTCAGTGC 216  
DB 121 TCTTTCGGATGCGACAGTGGATGGGACAGGCGACAGGCGACACGACATTCAGTGC 180  
QY 217 AGCTCAGTGGGAAAGGCTGGGGGAGGTGTATATAAGAGTACCGAGACTGGGCACTACT 276  
DB 181 AGCTCAGTGGGAAAGGCTGGGGGAGGTGTATATAAGAGTACCGAGACTGGGCACTACT 240  
QY 277 TGGCATGACACCGAGCGGCTTTTACGGCTCACAGACACCAATGAGGAATGTTGT 336  
DB 241 TGGCTATGACACCGAGCGGCTTTTACGGCTCACAGACACCAATGAGGAATGTTGT 300  
QY 337 TCTTGGAAAGGCTGGAGGACCACTTACCACTATATATCAAGAGCATGACAGGA 396  
DB 301 TCTTGGAAAGGCTGGAGGACCACTTACCACTATATATCAAGAGCATGACAGGA 360  
QY 397 AGAATGTTGTTGGCTCTCAGAGAAATGGGAGCTGCAAAAGCGGCTCTTAACTACT 456  
DB 361 AGAATGTTGTTGGCTCTCAGAGAAATGGGAGCTGCAAAAGCGGCTCTTAACTACT 420  
QY 457 ATGGCCAGAAAGCAATCTGTTCTCTCCCTGCGAGTCTCTCTGATTAAG 508  
DB 421 ATGGCCAGAAAGCAATCTGTTCTCTCCCTGCGAGTCTCTCTGATTAAG 472  
RESULT 14  
ABV78179  
ID ABV78179 standard; DNA; 468 BP.  
XX  
AC ABV78179;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Human DNA SEQ ID NO 63.  
XX  
RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic;  
virucide; protozoacide; gene; ds.  
Homo sapiens.  
WO200255693-A2.  
XX  
FD 18-JUL-2002.  
XX  
PF 09-JAN-2002; 2002WO-EF000152.  
XX  
PR 09-JAN-2001; 2001DE-01000586.  
PR 26-OCT-2001; 2001DE-01055280.  
PR 29-NOV-2001; 2001DE-01058411.  
PR 07-DEC-2001; 2001DE-01060151.  
XX  
PA (RIBO-) RIBOPHARMA AG.  
XX  
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;  
XX  
DR WPI; 2002-590671/63.  
XX  
Inhibiting expression of target gene, useful e.g. for inhibiting  
PT oncogenes, by administering double-stranded RNA complementary to the  
PT target and having an overhang.  
XX  
PS Claim 10; Page 147; 203pp; German.

XX The invention relates to inhibiting expression of a target gene (I) in a  
CC cell by introducing an inhibitory RNA (dsRNA) having a double-stranded  
CC structure of at most 49 consecutive bases. At least part of one strand  
CC (asi) of dsRNA is complementary to (I) and at least one end of dsRNA1  
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the  
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.  
CC in humans, also genes in plasmid or in viruses or viroids that are  
CC pathogenic for humans, animals or plants. Introducing an overhang into  
CC dsRNA greatly increases effectiveness for inhibiting gene expression,  
CC both in vivo and in vitro and also increases stability and thus the  
CC effective concentration inside the cell. The present sequence is that of  
CC a gene related to the invention  
XX  
SQ Sequence 468 BP; 131 A; 115 C; 126 G; 96 T; 0 U; 0 Other;  
Query Match 72.6%; Score 453.2; DB 5; Length 468;  
Best Local Similarity 99.4%; Pred. No. 2.2e-133;  
Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 39 ATGGCTGAAGGGGAATCACCACCTTCACAGCCCTGACCGAGAGTTTAACTGCTCCA 98  
DB 1 ATGGCTGAAGGGGAATCACCACCTTCACAGCCCTGACCGAGAGTTTAACTGCTCCA 60  
QY 99 GGGGAATTACAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCACTTCTGAGGATC 158  
DB 61 GGGGAATTACAGAGCCCAAACTCTCTACTGTAGCAACGGGGGCACTTCTGAGGATC 120  
QY 159 CTTCGGATGGCACAGTGGATGGGACAGGCGACAGGCGACCACTTCAGCTGCAG 218  
DB 121 CTTCGGATGGCACAGTGGATGGGACAGGCGACAGGCGACCACTTCAGCTGCAG 180  
QY 219 CTCAGTGGGAAAGGCTGGGGGAGGTGTATATAAGAGTACCGAGACTGGGCACTTTG 278  
DB 181 CTCAGTGGGAAAGGCTGGGGGAGGTGTATATAAGAGTACCGAGACTGGGCACTTTG 240  
QY 279 GCCTGACACACGAGGCTTTTATACGGCTCACAGACCACTTAAAGAGTATGTTGTC 338  
DB 241 GCCTGACACACGAGGCTTTTATACGGCTCACAGACCACTTAAAGAGTATGTTGTC 300  
QY 339 CTGGAAGGCTGGAGGAGACCACTTACCACTTATATCAAGAGCATGACAGGAAG 398  
DB 301 CTGGAAGGCTGGAGGAGACCACTTACCACTTATATCAAGAGCATGACAGGAAG 360  
QY 399 AATTGTTTGTGGCTCAAGAGAAATGGGAGCTGCAAGCGGCTCTTAAACTCACTAT 458  
DB 361 AATTGTTTGTGGCTCAAGAGAAATGGGAGCTGCAAGCGGCTCTTAAACTCACTAT 420  
QY 459 GCGGAGAAAGCAATCTGTTCTCTCCCTGCGAGTCTCTCTGATTAA 506  
DB 421 GCGGAGAAAGCAATCTGTTCTCTCCCTGCGAGTCTCTCTGATTAA 468  
RESULT 15  
ABZ35755  
ID ABZ35755 standard; DNA; 468 BP.  
XX  
AC ABZ35755;  
XX  
DT 07-FEB-2003 (first entry)  
XX  
DE Human polynucleotide SEQ ID NO 63.  
XX  
KW Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;  
KW protozoacide; gene expression; antisense; tumour; infection; plasmid;  
KW virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;  
KW Hepatitis C virus; human papilloma virus; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10100588-A1.  
XX  
FD 18-JUL-2002.  
XX  
PF 09-JAN-2001; 2001DE-01000588.  
XX  
PR 09-JAN-2001; 2001DE-01000588.  
XX  
PA (RIBO-) RIBOPHARMA AG.

XX PI Kreutzer R, Limmer S, Rost S, Hadwiger P;  
XX WPI; 2002-683450/74.  
XX Inhibiting expression of target genes, useful e.g. for treating tumors,  
PT by introducing into cells two double-stranded RNAs that are complementary  
PT to the target.  
XX Claim 13; Page 44; 100pp; German.  
XX The invention relates to inhibiting expression of a target gene in a cell  
CC by introducing at least two oligonucleotides (dsRNAI and II), both  
CC with a double-stranded (ds) structure of at most 49 sequential nucleotide  
CC pairs. At least part of one strand (S1, S2) of the ds structures in each  
CC of dsRNAI and II are complementary to regions in the target gene. The  
CC method uses antisense inhibition of gene expression using double stranded  
CC RNA inhibition (RNAi). The method is particularly used to treat tumours  
CC or infections, especially by Plasmodium or viruses/viroids (pathogenic on  
CC humans, animals or plants). The method provides more effective inhibition  
CC of expression than known methods using a single dsRNA, even at very low  
CC concentrations. When dsRNA has at least one unpaired nucleotide at the  
CC end, stability (and thus effective concentration in the cell) is improved  
CC and efficiency can be increased further by pretreating the cells with  
CC interferon. The present sequence is that of a target DNA of the invention  
XX  
SQ Sequence 468 BP; 131 A; 115 C; 126 G; 96 T; 0 U; 0 Other;

Query Match 72.6%; Score 463.2; DB 6; Length 468;  
Best Local Similarity 99.4%; Pred. No. 2.2e-133;  
Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 39 ATGGCTCGAAGGAAATCCACCTTCACAGCCCTGACGAGAGTTTATCTGCCTCCA 98  
Db 1 ATGGCTCGAAGGAAATCCACCTTCACAGCCCTGACGAGAGTTTATCTGCCTCCA 60  
QY 99 GGAATATCAAGAGCCCAAACTCTCTACTGTAGCAAGGGGGCCACTTCTCGAGGATC 158  
Db 61 GCGAATATCAAGAGCCCAAACTCTCTACTGTAGCAAGGGGGCCACTTCTCGAGGATC 120  
QY 159 CTTCCGATGCGCAGGATGAGTGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 218  
Db 121 CTTCCGATGCGCAGGATGAGTGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
QY 219 CTCAGTCCGGAAGGCTGGGGGAGGTGTATATAAGAGTACCGAGATCGCCAGTACTTG 278  
Db 181 CTCAGTCCGGAAGGCTGGGGGAGGTGTATATAAGAGTACCGAGATCGCCAGTACTTG 240  
QY 279 GCGATGACACCGAGCGGCTTTTATCGCTCAGACACCAATAGGAGTGTCTTC 338  
Db 241 GCGATGACACCGAGCGGCTTTTATCGCTCAGACACCAATAGGAGTGTCTTC 300  
QY 339 CTGGAAGGCTGGAGAGAACCATTAACACCTATATATCCAGAGCATCGAGAGAG 398  
Db 301 CTGGAAGGCTGGAGAGAACCATTAACACCTATATATCCAGAGCATCGAGAGAG 360  
QY 399 AATTGGTTTGTGGCTCAGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 458  
Db 361 AATTGGTTTGTGGCTCAGAGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 420  
QY 459 GGCAGGAAGCAATCTGTCTTCTCCCTGCGAGTCTCTCTGATTAA 506  
Db 421 GGCAGGAAGCAATCTGTCTTCTCCCTGCGAGTCTCTCTGATTAA 468

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and is derived by analysis of the total score distribution.

SUMMARIES									
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3	470.6	73.8	8501	3	US-08-793-900-1		Sequence 1, Appli		
4	463.2	72.6	468	4	US-09-929-945-3		Sequence 3, Appli		
5	412.8	64.7	454	6	5175147-1		Patent No. 5175147		
6	361.5	56.7	450	6	5437995-1		Patent No. 5437995		
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8	357.8	56.1	454	4	US-09-451-905-14		Sequence 14, Appli		
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10	280.6	44.0	630	4	US-09-929-945-6		Sequence 6, Appli		
11	268.2	42.0	630	4	US-09-929-945-4		Sequence 4, Appli		
12	174.8	27.4	197	6	5514566-3		Patent No. 5514566		
13	165	25.9	261	1	US-08-070-165F-1		Sequence 1, Appli		
14	165	25.9	261	2	US-08-885-418-1		Sequence 1, Appli		
15	159.2	25.0	270	6	5514566-1		Patent No. 5514566		
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21	128.2	20.1	465	1	US-08-177-502-3		Sequence 3, Appli		
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28	120.8	18.9	441	6	5464943-13		Patent No. 5464943		
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34	120.8	18.9	528	3	US-09-105-678A-2		Sequence 2, Appli		
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## RESULT 1

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Query Match	86.2%	Score 549.8	DB 3	Length 638
Best Local Similarity	98.5%	Pred. No. 2.8e-166		
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303	QY	TAGGGCTACAGACACCAATATGAGANTGTGTCTCGAAGAGCGCTCGAGGACCAAT	362
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415	QY	AATGGGAGCTGCAAAACGCGGTCCTCAAAACTCACTATATGGCCAGAGAAGCAATCTTTCTTC	482
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423	QY	CCCCCTGCCAGTCTCTTCTGATTAAGAAGATCTGTTCCT - GGTTGTTGACCACTCCAGAGAAG	541
	DB	CCCCCTGCCAGTCTCTTCTGATTAAGAAGATCTGTCTGGGTTGTGACCACTCCAGAGAAG	594
483	QY	TTTCGAGGGGCTCTCACTCTGGTTGACCCCAAAAATGTTCCTTTGA	586
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RESULT 2

US-09-023-655-1390

US-09-023-655-1390, Application US/09023655

Patent No. 6607879

GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G.

APPLICANT: Susan G. Stuart

APPLICANT: Jeffrey J. Seilhamer

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

TITLE OF INVENTION: EXPRESSION

NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,655

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1390:

SEQUENCE CHARACTERISTICS:

LENGTH: 490 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: g396163

US-09-023-655-1390

Query Match	76.1%	Score 485.2	DB 4	Length 490																				
Best Local Similarity	99.4%	Prod. NO. 1.3e-145																						
Matches 487	Conservative 13	Mismatches 45	Indels 0	Gaps 0																				
<table border="0"> <tr> <td>QY</td> <td>29</td> <td>CTGCTGAGCCATGCTGAAAGGGGAAATCAACACCTTCTACAGCCCTGACCGAGAAAGTTTAA</td> <td>88</td> </tr> <tr> <td></td> <td></td> <td>     </td> <td></td> </tr> <tr> <td>Db</td> <td>1</td> <td>CTGCTGAGCCATGCTGAAAGGGGAAATCAACACCTTCTACAGCCCTGACCGAGAAAGTTTAA</td> <td>60</td> </tr> <tr> <td></td> <td></td> <td>     </td> <td></td> </tr> <tr> <td>QY</td> <td>89</td> <td>TCTSCCTTCCACGGGAATTTACACGAAGGCCAAACTCTCTACTGTATGACACAGGGGGCCACTT</td> <td>148</td> </tr> </table>					QY	29	CTGCTGAGCCATGCTGAAAGGGGAAATCAACACCTTCTACAGCCCTGACCGAGAAAGTTTAA	88					Db	1	CTGCTGAGCCATGCTGAAAGGGGAAATCAACACCTTCTACAGCCCTGACCGAGAAAGTTTAA	60					QY	89	TCTSCCTTCCACGGGAATTTACACGAAGGCCAAACTCTCTACTGTATGACACAGGGGGCCACTT	148
QY	29	CTGCTGAGCCATGCTGAAAGGGGAAATCAACACCTTCTACAGCCCTGACCGAGAAAGTTTAA	88																					
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QY	89	TCTSCCTTCCACGGGAATTTACACGAAGGCCAAACTCTCTACTGTATGACACAGGGGGCCACTT	148																					

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Qy 149 CCGTGGAGATCTCTCCGGATGGGCAAGTGGATGGGACAAAGGACAGGAGGACGACACAT 208  
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Qy 329 ATGTTTCTCTGGAAAGGCTGGAGGAGCACTTATCAACACTATATATCAAGAGCA 388  
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Qy 389 TGCAGAGAGAAATGGTTTGGCTCAAGAGAAATGGGAGCTGCAAAAGCGGGTCTTAA 448  
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Qy 449 AACTCATATGGCCAGAGAACTTGTGTTCTGCGCCCTGCCAGTCTTCTCATTAAG 508  
Db 421 GACTCATATGGCCAGAGAACTTGTGTTCTGCGCCCTGCCAGTCTTCTCATTAAG 480  
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Db 481 AGATCTGTC 490

RESULT 3  
US-08-793-900-1

; Sequence 1, Application US/08793900  
; Patent No. 6143518  
; GENERAL INFORMATION:  
; APPLICANT: CAMERON, Beatrice  
; APPLICANT: CHOUZET, Joel  
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF RECOMBINANT  
; TITLE OF INVENTION: PROTEINS, PLASMIDS AND MODIFIED CELLS  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, Mailstop 3043  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,900  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR95/01178  
; FILING DATE: 14-SEP-1995  
; APPLICATION NUMBER: FR 94/11049  
; FILING DATE: 16-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky Esq., Martin F.  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: ST94069-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3816  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8501 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: cDNA  
US-08-793-900-1

Query Match 73.8%; Score 470.6; DB 3; Length 8501;  
Best Local Similarity 99.2%; Pred. No. 2.8e-140;  
Matches 473; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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Qy 219 CTCAGTGGCGAAGCGTGGGGAGGCTGTATATTAAGAGTACCGAGACTGGCCAGTACTTG 278  
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Qy 279 GCCATGACACACCGGCGCTTTTATACGGCTCAGACACCAAAATGAGAAATGTTGTTTC 338  
Db 348 GCCATGACACACCGGCGCTTTTATACGGCTCAGACACCAAAATGAGAAATGTTGTTTC 407  
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Qy 399 AATTGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAAAAGCGGCTCTTAAACTCATAT 458  
Db 468 AATTGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAAAAGCGGCTCTTAAACTCATAT 527  
Qy 459 GCGCAGAGAGCACTTGTGTTCTGCGCCCTGCCAGTCTTCTGATTAAGAGATCTG 515  
Db 528 GCGCAGAGAGCACTTGTGTTCTGCGCCCTGCCAGTCTTCTGATTAAGAGATCTG 584

RESULT 4

US-09-929-945-3  
; Sequence 3, Application US/09929945  
; Patent No. 6642026  
; GENERAL INFORMATION:  
; APPLICANT: Stegmann, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155  
; FILE REFERENCE: CVCENG.008A  
; CURRENT APPLICATION NUMBER: US/09/929,945  
; CURRENT FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-929-945-3

Query Match 72.6%; Score 463.2; DB 4; Length 468;  
Best Local Similarity 99.4%; Pred. No. 1.4e-138;  
Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 39 ATGGCTGAAGGGGAAATCACCACTTTCACAGCCCTGACCGAGAGTAAATCTGCTCCA 98  
Db 1 ATGGCTGAAGGGGAAATCACCACTTTCACAGCCCTGACCGAGAGTAAATCTGCTCCA 60  
Qy 99 GCGAATTACAGAGAGCCCAAACTCTCTACTGTAGCAAGCGGGGCGCACTTCTGAGGATC 158  
Db 61 GGGAAATTACAGAGAGCCCAAACTCTCTACTGTAGCAAGCGGGGCGCACTTCTGAGGATC 120  
Qy 159 CTTCCGGATGGCAGATGGATGGGACAAAGGACAGGAGCGGACGACATTTAGCTGGAG 218  
Db 121 CTTCCGGATGGCAGATGGATGGGACAAAGGACAGGAGCGGACGACATTTAGCTGGAG 180  
Qy 219 CTCAGTGGCGAAGCGTGGGGAGGCTGTATATTAAGAGTACCGAGACTGGCCAGTACTTG 278  
Db 181 CTCAGTGGCGAAGCGTGGGGAGGCTGTATATTAAGAGTACCGAGACTGGCCAGTACTTG 240

QY 279 GCATGGACGACGCGGCTTTTATACGGCTCAGACACCAATCAGGAATTTGTTTC 338  
DB 241 GCATGGACGACGCGGCTTTTATACGGCTCAGACACCAATCAGGAATTTGTTTC 300  
QY 339 CTGGAAGGCTGGAGGAGAACCAATTAACACCTATATATCCAAAGAGCATGACAGAG 398  
DB 301 CTGGAAGGCTGGAGGAGAACCAATTAACACCTATATATCCAAAGAGCATGACAGAG 360  
QY 399 AATTGGTTTGGCTCAGAGAGATGGAGGCTCAACGGGCTTAAACTCACTAT 458  
DB 361 AATTGGTTTGGCTCAGAGAGATGGAGGCTCAACGGGCTTAAACTCACTAT 420  
QY 459 GGCCAGAAAGCAATCTGTTTCTCCCGCTCCAGTCTCTCTGATTAA 506  
DB 421 GGCCAGAAAGCAATCTGTTTCTCCCGCTCCAGTCTCTCTGATTAA 468

RESULT 5  
5175147-1  
; PATENT NO. 5175147  
; APPLICANT: FOLKMAN, MOSES J.; KATO, KOICHI  
; TITLE OF INVENTION: ACID-RESISTANT FGF COMPOSITION AND METHOD  
; OF TREATING ULCERATING DISEASES OF THE GASTROINTESTINAL TRACT  
; NUMBER OF SEQUENCES: 19  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/382,263  
; FILING DATE: 20-JUL-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 234,966  
; FILING DATE: 19-AUG-1988  
; SEQ ID NO:1:  
; LENGTH: 454  
5175147-1

Query Match 64.7%; Score 412.8; DB 6; Length 454;  
Best Local Similarity 96.1%; Pred. No. 1.9e-122;  
Matches 423; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 71 CTGACCGAGAGTCTTAATCTGCTCCAGGGAATTAACAGACCCCAACTCTCTACTG 130  
DB 4 CTTACTTGCATGTTTAAATCTGCTCCCGGAATTAACAGACCCCAACTCTCTACTG 63  
QY 131 TAGCAACGGGGCCACTTCTGAGGATCTTCCGGATGGACAGTGGATGGACAGGGA 190  
DB 64 CAGCAACGGGGCCACTTCTGAGGATCTTCCGGATGGACAGTGGATGGACAGGGA 123  
QY 191 CAGGAGCCAGCAGCATTCAGCTCAGCTCAGTGCAGGAAGCTGGGGAGGTGTATAT 250  
DB 184 AAAGAGTACCGAGCTGCGGCAATTCAGTGGCAATTCAGCAGCGGCTTTTATACGGCTC 243  
QY 311 ACAGACCCCAATCAGGAATGTTTCTTGGAAAGGCTGGAGGAGACCAATTAACAC 370  
DB 244 ACAGACCCCAATCAGGAATGTTTCTTGGAAAGGCTGGAGGAGACCAATTAACAC 303  
QY 371 CTATATATCCAAAGCATGCGAGAGAAATTTGTTTGGCTTCAAGAAATGGGAG 430  
DB 304 CTATATATCCAAAGCATGCGAGAGAAATTTGTTTGGCTTCAAGAAATGGGAG 363  
QY 431 CTGGAAGCGGCTTCAAACTCACTATGCGAGAGAAATTTGTTTGGCTTCAAGAAATGGGAG 490  
DB 364 CTGGAAGCGGCTTCAAACTCACTATGCGAGAGAAATTTGTTTGGCTTCAAGAAATGGGAG 423  
QY 491 AGTCTCTCTGATTAAAGAG 510  
DB 424 AGTCTCTCTGATTAAAG 443

RESULT 6  
5437995-1  
; PATENT NO. 5437995  
; APPLICANT: ICHIMORI, YUZO; KONDO, KOICHI; IGARASHI, KOICHI;  
; SENDO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AGAINST AN ACIDIC  
; FGF PROTEIN AND HYBRIDOMA FOR ITS PRODUCTION

; NUMBER OF SEQUENCES: 3  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/26,257  
; FILING DATE: 04-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 588,343  
; FILING DATE: 26-SEP-1990  
; SEQ ID NO:1:  
; LENGTH: 450  
5437995-1

Query Match 56.7%; Score 361.6; DB 6; Length 450;  
Best Local Similarity 94.8%; Pred. No. 4.9e-106;  
Matches 417; Conservative 0; Mismatches 19; Indels 4; Gaps 4;

QY 71 CTGACCGAGAGTCTTAATCTGCTCCAGGGAATTAACAGACCCCAACTCTCTACTG 130  
DB 4 CTTACTTGCATGTTTAAATCTGCTCCCGGAATTAACAGACCCCAACTCTCTACTG 63  
QY 131 TAGCAACGGGGCCACTTCTGAGGATCTTCCGGATGGACAGTGGATGGACAGGGA 190  
DB 64 CAGCAACGGGGCCACTTCTGAGGATCTTCCGGATGGACAGTGGATGGACAGGGA 123  
QY 191 CAGGAGCCAGCAGCATTCAGCTCAGCTCAGTGCAGGAAGCTGGGGAGGTGTATAT 250  
DB 124 CAGGA-CGACAGCAGCATTCAGCTCAGCTCAGTGCAGGAAGCTGGGGAGGTGTATAT 182  
QY 251 AAAGAGTACCGAGCTGCGGCAATTCAGTGGCAATTCAGCAGCGGCTTTTATACGGCTC 310  
DB 183 AAAGAGTACCGAGCTGCGGCAATTCAGTGGCAATTCAGCAGCGGCTTTTATACGGCTC 241  
QY 311 ACAGACCCCAATCAGGAATGTTTCTTGGAAAGGCTGGAGGAGACCAATTAACAC 370  
DB 242 ACAGACCCCAATCAGGAATGTTTCTTGGAAAGGCTGGAGGAGACCAATTAACAC 301  
QY 371 CTATATATCCAAAGCATGCGAGAGAAATTTGTTTGGCTTCAAGAAATGGGAG 430  
DB 302 CTATATATCCAAAGCATGCGAGAGAAATTTCTTTTGGCTTCAAGAAATGGGAG 360  
QY 431 CTGGAAGCGGCTTCAAACTCACTATGCGAGAGAAATTTGTTTGGCTTCAAGAAATGGGAG 490  
DB 361 CTGGAAGCGGCTTCAAACTCACTATGCGAGAGAAATTTGTTTGGCTTCAAGAAATGGGAG 419  
QY 491 AGTCTCTCTGATTAAAGAG 510  
DB 420 AGTCTCTCTGATTAAAG 439

RESULT 7  
US-09-030-613-14  
; Sequence 14, Application US/09030613  
; Patent No. 6083706  
; GENERAL INFORMATION:  
; APPLICANT: Florkiewicz, Robert Z.  
; APPLICANT: Baird, J. Andrew  
; TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,613  
; FILING DATE: 25-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6083706tenburg Ph.D., Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 760100.418C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900

159 CTTCCGATGGGACAGTGGATGGGACAGGACAGGAG-CGACCAGCAGCAATTCAGCTGCA 217  
121 CTTCCGATGGGACAGTGGATGGGACAGGACAGGAGCCGACAGCAGCAATTCAGCTGCA 180  
218 GCTCAGTGGGAAAGCGTGGGGAGGTGTATATTAAGAGTACCGAGCTGGCCAGTAC-T 276  
181 ACTCAGTGGGAAAGCGTGGGGAGGTGTATATTAAGAGTACCGAGCTGGCCAGTACTT 240  
277 TGGCATGACACACCGAGCGGCTTTTATACGGCTCACAGACACCAAAATGAGGAATGTTGT 336  
241 TGGCATGACACACCGAGCGGCTTTTATACGGCTCACAGACACCAAAATGAGGAATGTTGT 300  
337 TCTTGAAAGGCTGGAGAG-AACCATTAACACCTTATATTCAGAGCATGCGAG 395  
301 TCTTGAAAGGCTGGAGAGAACCATTAACACCTTATATTCAGAGCATGCGAG 360  
396 AAGAAATGTTGTTGGCTTCAAGAGAAATGGAGCTGCAAAACGGGTCTTAAACTCAC 455  
361 AAGAAATGTTGTTGGCTTCAAGAGAAATGGAGCTGCAAAACGGGTCTTAAACTCAC 400  
456 TATGCCAGAAAGCAATCTTGTCTTCCCTGCGAGTCTCTTCTGATTA 506  
401 TATGCCAGAAAGCAATCTTGTCTTCCCTGCGAGTCTCTTCTGATTA 451

RESULT 9  
US-09-929-945-1  
; Sequence 1, Application US/09929945  
; Patent No. 6642026  
; GENERAL INFORMATION:  
; APPLICANT: Stegmann, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svetlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozlanov, Oleksandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
; FILE REFERENCE: CVGENG.008A  
; CURRENT APPLICATION NUMBER: US/09/929,945  
; CURRENT FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq For Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 630  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized sequence for human acidic  
; OTHER INFORMATION: Fibroblast Growth Factor (155 amino acids) using  
; OTHER INFORMATION: preferred codons for E. coli  
; NAME/KEY: CDS  
; LOCATION: (122)...(590)  
US-09-929-945-1

Query Match 49.2%; Score 314.2; DB 4; Length 630;  
Best Local Similarity 79.2%; Pred. No. 9,2e-91;  
Matches 373; Conservative 0; Mismatches 98; Indels 0; Gaps 0;  
39 ATGCTGAGGGGAAATCAACCTTCAAGCCCTGACCGAGAGTTTAACTGCTCCA 98  
122 ATGCTGAGGGGAAATCAACCTTCAAGCCCTGACCGAGAGTTTAACTGCTCCA 181  
99 GGGAAATTACAAAGAGCCCAACTCTCTACTGTAGCAAGCGGGGCCACTTCTGAGGATC 158  
182 GGGAAATTACAAAGAGCCCAACTCTCTACTGTAGCAAGCGGGGCCACTTCTGAGGATC 241  
159 CTTCCGATGGGACAGTGGATGGGACAGGACAGGAGCCGACAGCAGCAATTCAGCTGCA 218  
242 CTTCCGATGGGACAGTGGATGGGACAGGAGCCGACAGCAGCAATTCAGCTGCA 301  
219 CTTCCGATGGGACAGTGGATGGGACAGGAGCCGACAGCAGCAATTCAGCTGCA 278  
302 CTTCCGATGGGACAGTGGATGGGACAGGAGCCGACAGCAGCAATTCAGCTGCA 361  
279 GCGAATGACACCGAGCGGCTTTTATACGGCTCACAGACACCAAAATGAGGAATGTTGT 338  
362 GCGAATGACACCGAGCGGCTTTTATACGGCTCACAGACACCAAAATGAGGAATGTTGT 421  
339 CTGGAAGGCTGGAGAGAACCTTCAACACTTATATTCAGAGCATGCGAGAG 398

TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 454 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-030-613-14  
Query Match 56.1%; Score 357.8; DB 3; Length 454;  
Best Local Similarity 91.5%; Pred. No. 8.2e-105;  
Matches 431; Conservative 0; Mismatches 17; Indels 23; Gaps 4;  
39 ATGCTGAGGGGAAATCAACCTTCAAGCCCTGACCGAGAGTTTAACTGCTCCA 98  
1 ATGCTGAGGGGAAATCAACCTTCAAGCCCTGACCGAGAGTTTAACTGCTCCA 60  
99 GGGAAATTACAAAGAGCCCAACTCTCTACTGTAGCAAGCGGGGCCACTTCTGAGGATC 158  
61 GGGAAATTACAAAGAGCCCAACTCTCTACTGTAGCAAGCGGGGCCACTTCTGAGGATC 120  
159 CTTCCGATGGGACAGTGGATGGGACAGGACAGGAG-CGACCAGCAGCAATTCAGCTGCA 217  
121 CTTCCGATGGGACAGTGGATGGGACAGGAGCCGACAGCAGCAATTCAGCTGCA 180  
218 GCTCAGTGGGAAAGCGTGGGGAGGTGTATATTAAGAGTACCGAGCTGGCCAGTAC-T 276  
181 ACTCAGTGGGAAAGCGTGGGGAGGTGTATATTAAGAGTACCGAGCTGGCCAGTACTT 240  
277 TGGCATGACACACCGAGCGGCTTTTATACGGCTCACAGACACCAAAATGAGGAATGTTGT 336  
241 TGGCATGACACACCGAGCGGCTTTTATACGGCTCACAGACACCAAAATGAGGAATGTTGT 300  
337 TCTTGAAAGGCTGGAGAG-AACCATTAACACCTTATATTCAGAGCATGCGAG 395  
301 TCTTGAAAGGCTGGAGAGAACCATTAACACCTTATATTCAGAGCATGCGAG 360  
396 AAGAAATGTTGTTGGCTTCAAGAGAAATGGAGCTGCAAAACGGGTCTTAAACTCAC 455  
361 AAGAAATGTTGTTGGCTTCAAGAGAAATGGAGCTGCAAAACGGGTCTTAAACTCAC 400  
456 TATGCCAGAAAGCAATCTTGTCTTCCCTGCGAGTCTCTTCTGATTA 506  
401 TATGCCAGAAAGCAATCTTGTCTTCCCTGCGAGTCTCTTCTGATTA 451

RESULT 8  
US-09-451-905-14  
; Sequence 14, Application US/09451905  
; Patent No. 6306613  
; GENERAL INFORMATION:  
; APPLICANT: Robert Z. Florkiewicz  
; APPLICANT: Andrew Baird  
; APPLICANT: Dale E. Warnock  
; TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT  
; TITLE OF INVENTION: AND METHODS FOR IDENTIFYING AND USING THE SAME  
; FILE REFERENCE: 200124.402C4  
; CURRENT APPLICATION NUMBER: US/09/451,905  
; CURRENT FILING DATE: 1999-12-01  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 454  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-451-905-14

Query Match 56.1%; Score 357.8; DB 4; Length 454;  
Best Local Similarity 91.5%; Pred. No. 8.2e-105;  
Matches 431; Conservative 0; Mismatches 17; Indels 23; Gaps 4;  
39 ATGCTGAGGGGAAATCAACCTTCAAGCCCTGACCGAGAGTTTAACTGCTCCA 98  
1 ATGCTGAGGGGAAATCAACCTTCAAGCCCTGACCGAGAGTTTAACTGCTCCA 60  
99 GGGAAATTACAAAGAGCCCAACTCTCTACTGTAGCAAGCGGGGCCACTTCTGAGGATC 158  
61 GGGAAATTACAAAGAGCCCAACTCTCTACTGTAGCAAGCGGGGCCACTTCTGAGGATC 120

Db 422 CTAGAAAGACTAGAAAGAAACCTTACACAGCTACATATCGAAAAACATCGAGAG 481  
Qy 399 AATTGGTTTGTGGCTTCAAGAGATGGGAGCTGCAAAACGGGTCTTAAATCACTAT 458  
Db 482 AACTGGTTGTAGGCTTAAAAAAATGGTCTCTGTAAGCGTGGACCGAGCTCACTAT 541  
Qy 459 GCGCAGAAAGCAATCTGTTCTCCCGCTCCAGCTCTCTCTGATTAAGA 509  
Db 542 GCGCAAGAGGCTATCTGTTCTCGCACTACCACTAGCTGAGCTCGGACTAAGA 592

RESULT 10

US-09-929-945-6

Sequence 6, Application US/09929945

Patent No. 6642026

GENERAL INFORMATION:

APPLICANT: Stegmann, Thomas

APPLICANT: Kordyum, Vitaliy A.

APPLICANT: Chernykh, Svitlana I.

APPLICANT: Slavchenko, Iryna Yu.

APPLICANT: Vozianov, Oleksandr

TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT

TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155

FILE REFERENCE: CVGENG-008A

CURRENT APPLICATION NUMBER: US/09/929,945

CURRENT FILING DATE: 2001-08-15

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6

LENGTH: 630

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Chemically synthesized sequence for human acidic

OTHER INFORMATION: Fibroblast Growth Factor (140 amino acids) using

OTHER INFORMATION: preferred codons for E. coli

NAME/KEY: CDS

LOCATION: (122)...(544)

US-09-929-945-6

Query Match 44.0%; Score 280.6; DB 4; Length 630;  
Best Local Similarity 78.2%; Pred. No. 5.4e-80;  
Matches 337; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

Qy 79 AGAGTTTATCTGCTCCAGGGAATACAGAGCCCAAACTCTCTCTAGTACGACG 138  
Db 120 ATATGTTTAACTTCCGCGCGGAATACAAAAACCAAGCTTCTTCTGAGTAAAG 179  
Qy 139 GGGCCACTTCTGAGATCTCTCCGATGGCAGATGGATGGAGGAGGACAGAGCG 198  
Db 180 GAGGACACTTCTCGCAATCTCGCAGATGGCAGATGGAGTGGGACTCGCTCCG 239  
Qy 199 ACCAGCATTCAGCTCAGCTCAGTGGGAGGAGGAGGAGGAGTATATAAGAGTA 258  
Db 240 ACCAGCATTCAGCTCAGCTCAGTGGGAGGAGGAGGAGGAGTATATAAGAGTA 299  
Qy 259 CCGAGCTGGCCAGTACTTGGCCATGACACCGAGCGGGCTTTTATAGGCTCAGAGAC 318  
Db 300 CCGAGCTGGCCAGTACTTGGCCATGACACCGAGCGGGCTTCTGTATGGCTCAGAGAC 359  
Qy 319 CAATGAGGAGTGTGTTCTCGAAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAG 378  
Db 360 CTAGCAGAGAGTGTGTTCTTAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 419  
Qy 379 CCAGAAGCATCAGAGAGAGATGGTTTGTGGCTTCAAGAGAGATGGAGGAGGAGGAG 438  
Db 420 CGAAAAACATCAGAGAGAGATGGTTTGTAGGCTTAAAAAAATGGTCTCTTAAGC 479  
Qy 439 GGGTCTTAACTCAGTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 498  
Db 480 GTGGACACCGGACTCAGTATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 539  
Qy 499 CTGATTAAGA 509  
Db 540 CCGACTAAGA 550

RESULT 11

5514566-3

US-09-929-945-4

Sequence 4, Application US/09929945

Patent No. 6642026

GENERAL INFORMATION:

APPLICANT: Stegmann, Thomas

APPLICANT: Kordyum, Vitaliy A.

APPLICANT: Chernykh, Svitlana I.

APPLICANT: Slavchenko, Iryna Yu.

APPLICANT: Vozianov, Oleksandr

TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT

TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155

FILE REFERENCE: CVGENG-008A

CURRENT APPLICATION NUMBER: US/09/929,945

CURRENT FILING DATE: 2001-08-15

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 630

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Chemically synthesized sequence for human acidic

OTHER INFORMATION: Fibroblast Growth Factor (134 amino acids) using

OTHER INFORMATION: preferred codons for E. coli

NAME/KEY: CDS

LOCATION: (122)...(526)

US-09-929-945-4

Query Match 42.0%; Score 268.2; DB 4; Length 630;  
Best Local Similarity 78.5%; Pred. No. 5.1e-76;  
Matches 321; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Qy 101 GAATTCACAGAGCCCAAACTCTCTCTAGTACGAGGAGGAGGAGGAGGAGGAGGAG 160  
Db 124 GAATTCACAAAAACCAAGCTTCTTCTGCTAGTACGAGGAGGAGGAGGAGGAGGAG 183  
Qy 161 TCGGATGGCAGATGGATGGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 220  
Db 184 GCGAGATGGCAGATGGAGTGGGACTCGGATCGCTCCGACGACACATTCAGCTGCAACT 243  
Qy 221 CAGTCGCGAAGCGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 280  
Db 244 CTCGCGCGAAGCGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 303  
Qy 281 CATGACACCGCGGCTTTTATAGGCTCAGACAGACCAAAATGAGGAATGTTGTTCT 340  
Db 304 CATGACACCGATGGGCTTCTGTATGGCTCAGACAGCGCTTACGAGAGATGCTGTTCT 363  
Qy 341 GGAAGGCTGGAGAGAACCTTACACACTATATATCCAGAGAGGAGGAGGAGGAGGAG 400  
Db 364 AGAAGAGTGAAGAAAAACCTTACACACTATATATCCAGAAAAACATCGAGAGAG 423  
Qy 401 TTGGTTGTTGGCTCAAGAGAGATGGGAGCTGCAAAACGGGCTCTTAAAACTCCTATGG 460  
Db 424 CTGGTTGTTAGGCTTAAAAAAATGGTTCCTGTAAGCGTGGACCAACGAGCTCCTATGG 483  
Qy 461 CCGAAGCAATCTTGTCTTCCCGCTGCGAGTCTCTCTGATTAAAGA 509  
Db 484 CCAAGAGCTATCTTGTCTGCGCACTACCAAGTGAAGCTCGGACTAAGA 532

RESULT 12

5514566-3

Patent No. 5514566

APPLICANT: FIDES, JOHN C.; ABRAHAM, JUDITH A.

TITLE OF INVENTION: METHODS OF PRODUCING RECOMBINANT

FIBROBLASTS GROWTH FACTORS

NUMBER OF SEQUENCES: 21

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/417,022

FILING DATE: 05-APR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 809,163

FILING DATE: 16-DEC-1985

APPLICATION NUMBER: 775,521

FILING DATE: 12-SEP-1985

SEQ ID NO:3

LENGTH: 197

5514566-3

Query Match 27.4%; Score 174.8; DB 6; Length 197;  
Best Local Similarity 98.9%; Pred. No. 2.3e-46;  
Matches 176; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 36 GCGATGGCTGAAGCGGAATCCACCTTACAGCCCTGACCGAGAGTTTAACTTCGCT 95  
DB |||||  
7 GCGATGGCTGAAGCGGAATCCACCTTACAGCCCTGACCGAGAGTTTAACTTCGCT 66  
DB |||||  
QY 96 CCAGGGAATTACAGAGCCCAAACTCTCTACTGTAGCAAGCGGGGCGACTTCCTGAGG 155  
DB |||||  
67 CCAGGGAATTACAGAGCCCAAACTCTCTACTGTAGCAAGCGGGGCGACTTCCTGAGG 126  
DB |||||  
QY 156 ATCTTCGGATGGCAGAGTGGATGGACAGAGGACAGAGCGACACACATTCAGC 213  
DB |||||  
127 ATCTTCGGATGGCAGAGTGGATGGACAGAGGACAGAGCGACACACATTCAGC 184  
DB |||||

RESULT 13  
US-08-070-165F-1  
; Sequence 1, Application US/08070165F  
; Patent No. 5750365  
; GENERAL INFORMATION:  
; APPLICANT: Chiu, Ing-Ming  
; APPLICANT: Poulin, Matthew L  
; TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ing-Ming Chiu  
; STREET: S2052 Davis Medical Research Center, 480 West  
; STREET: 9th Avenue  
; CITY: Columbus  
; STATE: Ohio  
; COUNTRY: USA  
; ZIP: 43210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/070,165F  
; FILING DATE:  
; CLASSIFICATION: 435  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (614)-293-8093  
; TELEFAX: (614)-293-5631  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 261 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: No. 5750365ophthalmus viridescens  
; DEVELOPMENTAL STAGE: Adult  
; TISSUE TYPE: Brain  
; IMMEDIATE SOURCE:  
; CLONE: MP 75-1  
; POSITION IN GENOME:  
; UNITS: bp  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..261  
; PUBLICATION INFORMATION:  
; AUTHORS: Patrie, Kevin M  
; AUTHORS: Botelho, Mary Jane  
; AUTHORS: Ray, Subir K  
; AUTHORS: Mehta, Veela B  
; AUTHORS: Chiu, Ing-Ming  
; JOURNAL: J. Biol. Chem.  
; RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 261

Query Match 25.9%; Score 165; DB 1; Length 261;  
Best Local Similarity 77.0%; Pred. No. 3.8e-43;

Matches 201; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 90 CTGCTCCAGGGAATACAGAGCCCAAACTCTCTACTGTAGCAAGCGGGGCGACTTC 149  
DB |||||  
1 CTTCCTCAATGGAAACTACAGAGCCCTTAAGCTCTCTACTGTAGCAAGCGGGGCGACTTC 60  
DB |||||  
QY 150 CTGAGATCTCTCCGATGGCAGAGTGGATGGCAAGCGGACAGAGCGACCGACACATT 209  
DB |||||  
61 CTGCGAATCTCCAGATGGCGAGGTGGCGGACAGAGCGAGTACCCCATCATC 120  
DB |||||  
QY 210 CAGTCGAGCTCAGTCCGGAAGCGGTGGGGGAGGTCTATATAAGAGTACCGGAGCTGGC 269  
DB |||||  
121 CAGTCGAGCTTATSCAGAAAGCGGTGGCGGAGGTATATACATCAAGAGTCTGGAGACAGC 180  
DB |||||  
QY 270 CAGTACTTGGCCATGACACCGAGCGGCTTTTATAGGCTCAGACACCGAATAGAGAA 329  
DB |||||  
181 CAGTACTTGGCGATGGACGCGGCGAGTTATACGATCTCAATCACCAGCGAGAA 240  
DB |||||  
QY 330 TGGTTGTTCTCGAAAGCGCTG 350  
DB |||||  
241 TGGCTGTTCTTGGAGCGACTG 261  
DB |||||

RESULT 14  
US-08-885-418-1  
; Sequence 1, Application US/08885418  
; Patent No. 5925528  
; GENERAL INFORMATION:  
; APPLICANT: Chiu, Ing-Ming  
; APPLICANT: Poulin, Matthew L  
; TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ing-Ming Chiu  
; STREET: S2052 Davis Medical Research Center, 480 West  
; STREET: 9th Avenue  
; CITY: Columbus  
; STATE: Ohio  
; COUNTRY: USA  
; ZIP: 43210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/885,418  
; FILING DATE:  
; CLASSIFICATION: 435  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (614)-293-8093  
; TELEFAX: (614)-293-5631  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 261 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: No. 5925528ophthalmus viridescens  
; DEVELOPMENTAL STAGE: Adult  
; TISSUE TYPE: Brain  
; IMMEDIATE SOURCE:  
; CLONE: MP 75-1  
; POSITION IN GENOME:  
; UNITS: bp  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..261  
; PUBLICATION INFORMATION:  
; AUTHORS: Patrie, Kevin M  
; AUTHORS: Botelho, Mary Jane  
; AUTHORS: Ray, Subir K  
; AUTHORS: Mehta, Veela B  
; AUTHORS: Chiu, Ing-Ming  
; JOURNAL: J. Biol. Chem.

RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 261

Query Match 25.9%; Score 165; DB 2: Length 261;  
Best Local Similarity 77.0%; Pred. No. 3.8e-43;  
Matches 201; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
QY 90 CTGCTCCGAGGAAATTCACAGAGCCCAAACTCTCTCTAGTACGAGGGGCGCAATTC 149  
Db 1 CTTCCTCAATGGAAGCTTACCAAGAGCTTCTCTCTCTAGTACGAGGGGCGCAATTC 60  
QY 150 CTGAGGATCTCTCCGATGCGACAGTGGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 209  
Db 61 CTGGAATCTCTCCGATGCGAGTGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
QY 210 CAGCTGAGCTGAGTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 269  
Db 121 CAGCTGAGCTGAGTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180  
QY 270 CAGTACTTGGCAGTGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 329  
Db 181 CAGTACTTGGCAGTGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240  
QY 330 TGTCTGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 350  
Db 241 TGTCTGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 261

RESULT 15  
5514566-1  
; Patent No. 5514566  
; APPLICANT: FIDDES, JOHN C.; ABRAHAM, JUDITH A.  
; TITLE OF INVENTION: METHODS OF PRODUCING RECOMBINANT  
; FIBROBLASTS GROWTH FACTORS  
; NUMBER OF SEQUENCES: 21  
; CURRENT APPLICATION DATA:  
; FILING DATE: 05-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/417,022  
; FILING DATE: 05-APR-1995  
; APPLICATION NUMBER: 809,163  
; FILING DATE: 16-DEC-1985  
; APPLICATION NUMBER: 775,521  
; FILING DATE: 12-SEP-1985  
; SEQ ID NO: 1:  
; LENGTH: 270  
5514566-1

Query Match 25.0%; Score 159.2; DB 6: Length 270;  
Best Local Similarity 90.4%; Pred. No. 2.8e-41;  
Matches 170; Conservative 0; Mismatches 18; Indels 0; Gaps 0;  
QY 26 CAGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 85  
Db 9 CAGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 68  
QY 86 TATCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 145  
Db 69 TATCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 128  
QY 146 CTTCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 205  
Db 129 CTTCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 188  
QY 206 CATTCAGC 213  
Db 189 CAGTAAGC 196

Search completed: August 24, 2004, 20:52:02  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: August 24, 2004, 18:53:06 ; Search time 482 Seconds  
(without alignments)

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Title: US-10-022-554A-3  
Perfect score: 638  
Sequence: 1 gaatcggaagcgccacca.....cctgaatttgtaagcaactt 638  
Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0  
Searched: 3228839 seqs, 245606551 residues  
Total number of hits satisfying chosen parameters: 6457678  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 08  
Maximum Match 100%  
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12: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	601.8	94.3	4087	14	US-10-044-090-225 Sequence 225, Appli
2	549.8	86.2	638	10	US-09-902-460-3 Sequence 3, Appli
3	485.2	76.1	490	15	US-10-388-410-8 Sequence 6, Appli
4	485.2	76.1	490	17	US-10-641-643-1390 Sequence 1390, Ap
5	463.2	72.6	468	9	US-09-929-918-3 Sequence 3, Appli
6	463.2	72.6	468	15	US-10-280-864-3 Sequence 3, Appli
7	463.2	72.6	468	17	US-10-649-480-3 Sequence 3, Appli
8	463.2	72.6	468	15	US-10-280-864-3 Sequence 3, Appli
9	314.2	49.2	630	9	US-09-929-918-1 Sequence 1, Appli
10	314.2	49.2	630	9	US-09-929-918-1 Sequence 1, Appli
11	314.2	49.2	630	15	US-10-280-864-1 Sequence 1, Appli
12	314.2	49.2	630	17	US-10-649-480-1 Sequence 1, Appli
13	314.2	49.2	990	9	US-09-929-918-10 Sequence 1, Appli
14	302.8	47.5	3658	12	US-09-968-007A-133 Sequence 133, App
15	302.8	47.5	3658	12	US-09-968-007A-440 Sequence 440, App
16	280.6	44.0	630	9	US-09-929-918-6 Sequence 6, Appli
17	280.6	44.0	630	9	US-09-929-918-6 Sequence 6, Appli
18	280.6	44.0	630	15	US-10-280-864-6 Sequence 6, Appli
19	280.6	44.0	630	17	US-10-649-480-6 Sequence 6, Appli
20	268.2	42.0	630	9	US-09-929-918-4 Sequence 4, Appli
21	268.2	42.0	630	9	US-09-929-918-4 Sequence 4, Appli
22	268.2	42.0	630	15	US-10-280-864-4 Sequence 4, Appli
23	268.2	42.0	630	17	US-10-649-480-4 Sequence 4, Appli
c 24	201.4	31.6	580	9	US-09-864-761-13391 Sequence 13391, A
c 25	187.29	23.6	478	16	US-09-864-761-29943 Sequence 235, App
26	150.6	23.6	478	16	US-10-116-275-235 Sequence 5, Appli
27	128.8	20.2	483	9	US-09-826-210-1 Sequence 14, Appli
28	125	19.6	488	13	US-10-389-821-5 Sequence 14, Appli
29	120.8	18.9	432	13	US-10-432-585-14 Sequence 14, Appli

30 120.8 18.9 432 15 US-10-168-050-6 Sequence 6, Appli  
31 120.6 18.9 3877 15 US-10-131-985-6 Sequence 6, Appli  
32 120.6 18.9 6514 14 US-10-090-983-1 Sequence 1, Appli  
33 119.8 18.8 1374 10 US-09-775-964-26 Sequence 26, Appli  
34 119.8 18.8 16602 15 US-10-311-455-700 Sequence 700, App  
35 119.8 18.8 18357 17 US-10-433-793-114 Sequence 114, App  
36 119.2 18.7 441 9 US-09-802-365-3 Sequence 3, Appli  
37 119.2 18.7 441 9 US-09-886-856-3 Sequence 11, Appli  
38 119.2 18.7 444 15 US-10-155-785-11 Sequence 7, Appli  
39 119.2 18.7 474 9 US-09-802-365-7 Sequence 7, Appli  
40 119.2 18.7 474 9 US-09-886-856-7 Sequence 7, Appli  
41 119.2 18.7 489 9 US-09-934-706-11 Sequence 11, Appli  
42 119.2 18.7 489 13 US-10-344-634-7 Sequence 7, Appli  
43 119.2 18.7 630 16 US-10-408-415-4 Sequence 4, Appli  
44 119.2 18.7 1182 13 US-10-344-634-13 Sequence 13, Appli  
45 119.2 18.7 1527 9 US-09-934-706-15 Sequence 15, Appli

#### ALIGNMENTS

#### RESULT 1

US-10-044-090-225  
; Sequence 225, Application US/10044090  
; Publication No. US20020137081A1  
; GENERAL INFORMATION:  
; APPLICANT: Olga Bandman  
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION  
; FILE REFERENCE: PA-0028 US  
; CURRENT APPLICATION NUMBER: US/10/044\_090  
; CURRENT FILING DATE: 2002-01-09  
; NUMBER OF SEQ ID NOS: 850  
; SOFTWARE: PERL Program  
; SEQ ID NO 225  
; LENGTH: 4087  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc.feature  
; OTHER INFORMATION: Incyte ID No. US20020137081A1 336376.2  
US-10-044-090-225

Query Match 94.3%; Score 601.8; DB 14; Length 4087;  
Best Local Similarity 98.6%; Pred. No. 3.8e-192;  
Matches 628; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 3 ATTGGGAAGCGGCCCAACAGCAGCAGCTGCTGAGCCATGCTGAGGGGGAATCACCACC 62  
DB 470 AGTCTTGAAGAGCGGCCCAACAGCAGCAGCTGCTGAGCCATGCTGAGGGGGAATCACCACC 529  
QY 63 TTCACAGCCCTCAGCAGAGAGTTAATCTGCTCCAGGAGGANTTACAGAGCCCAAACTC 122  
DB 530 TTCACAGCCCTCAGCAGAGAGTTAATCTGCTCCAGGAGGANTTACAGAGCCCAAACTC 589  
QY 123 CTCTACTGTAGCAACGGGGGCCACTCTCTGAGGATCTCTCGGATGGCAGCTGGATGGG 182  
DB 590 CTCTACTGTAGCAACGGGGGCCACTCTCTGAGGATCTCTCGGATGGCAGCTGGATGGG 649  
QY 183 ACAAGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 242  
DB 650 ACAAGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 709  
QY 243 GTGTATATAAGAGTACCGAGAGTGGCCAGTACTTGGCCATGGACACCGAGCGGCTTTTA 302  
DB 710 GTGTATATAAGAGTACCGAGAGTGGCCAGTACTTGGCCATGGACACCGAGCGGCTTTTA 769  
QY 303 TACGGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 362  
DB 770 TACGGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 829  
QY 363 TACAACACCTATATATCAAGAGCAGTGCAGAGAGATTTGGTTTGTGGCTCCAGAGAG 422  
DB 830 TACAACACCTATATATCAAGAGCAGTGCAGAGAGATTTGGTTTGTGGCTCCAGAGAG 889  
QY 423 AATGGAGGCTGCAAGCGGGTCTTAAACTCATTATGGCCAGAGAGCAATCTTGTTC 482  
DB 890 AATGGAGGCTGCAAGCGGGTCTTAAACTCATTATGGCCAGAGAGCAATCTTGTTC 949  
QY 483 CCCTGCCAGTCTCTCTGATTAAAGAGATCTGTCT-GGTGTGACCACTCCAGAGAG 541

DB 950 CCCTGCCAGTCTCTCTGATTAAAGAGATCTGTGTGGGTGTGACCACTCCAGAGAG 1009  
QY 542 TTTCAGAGGGTCTCTCACTTGTGACCCCAAAATGTTCCCTTGACCATTTGGCTGCGCTA 601  
DB 1010 TTTCAGAGGGTCTCTCACTTGTGACCCCAAAATGTTCCCTTGACCATTTGGCTGCGCTA 1068  
QY 602 ACCCCAGCCCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 638  
DB 1069 ACCCCAGCCCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1105

#### RESULT 2

US-09-902-460-3  
; Sequence 3, Application US/09902460  
; Publication No. US20030040042A1  
; GENERAL INFORMATION:  
; APPLICANT: FIDDES, J.C.  
; ABRHAM, J.D.  
; TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH  
; FACTOR ANALOG  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/902.460  
; FILING DATE: 09-Jul-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/098.628  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lehnhardt, Susan K  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 21900-20089.10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 638 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 91...555  
; OTHER INFORMATION:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-902-460-3

Query Match 86.2%; Score 549.8; DB 10; Length 638;  
Best Local Similarity 98.5%; Pred. No. 6e-175;  
Matches 576; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 3 ATTGGGAAGCGGCCCAACAGCAGCAGCTGCTGAGCCATGCTGAGGGGGAATCACCACC 62  
DB 55 AGTCTTGAAGAGCGGCCCAACAGCAGCAGCTGCTGAGCCATGCTGAGGGGGAATCACCACC 114  
QY 63 TTCACAGCCCTCAGCAGAGAGTTAATCTGCTCCAGGGAATTACAAGAGCCCAAACTC 122  
DB 115 TTCACAGCCCTCAGCAGAGAGTTAATCTGCTCCAGGGAATTACAAGAGCCCAAACTC 174  
QY 123 CTCTACTGTAGCAACGGGGGCCACTCTCTGAGGATCTCTCGGATGGCAGCTGGATGGG 182  
DB 175 CTCTACTGTAGCAACGGGGGCCACTCTCTGAGGATCTCTCGGATGGCAGCTGGATGGG 234







; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155  
; FILE REFERENCE: CVGENG.008A  
; CURRENT APPLICATION NUMBER: US/10/280,864  
; CURRENT FILING DATE: 2002-10-24  
; PRIOR APPLICATION NUMBER: US/09/929,945  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-280-864-3

Query Match 72.6%; Score 463.2; DB 15; Length 468;  
Best Local Similarity 99.4%; Pred. No. 1e-145;  
Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 39 ATGGCTGAAGGGGAAATCACCACCTTTCACAGCCCTGACGAGAGTTTAACTGCTCCA 98  
Db 1 ATGGCTGAAGGGGAAATCACCACCTTTCACAGCCCTGACGAGAGTTTAACTGCTCCA 60  
QY 99 GGGAAATTACAAAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCCACTTCTGAGATC 158  
Db 61 GGGAAATTACAAAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCCACTTCTGAGATC 120  
QY 159 CTTCCGGATGGCAGCAGTGGATGGGACAGGAGGACAGGAGGACACGACATTCAGCTGCAG 218  
Db 121 CTTCCGGATGGCAGCAGTGGATGGGACAGGAGGACAGGAGGACACGACATTCAGCTGCAG 180  
QY 219 CTCAGTGGGAAAGCGTGGGAGAGTGTATATAAGAGTACCGAGCTGCGGACTGCTAT 278  
Db 181 CTCAGTGGGAAAGCGTGGGAGAGTGTATATAAGAGTACCGAGCTGCGGACTGCTAT 240  
QY 279 GCATGGACACCGCAGCGGCTTTTATACGGCTTCACACACCAATGAGAAATGTTGTC 338  
Db 241 GCATGGACACCGCAGCGGCTTTTATACGGCTTCACACACCAATGAGAAATGTTGTC 300  
QY 339 CTGGAAGGCTGGAGAGAACCAATTACCAACCTATATATCAAGAGCATGACAGAGAG 398  
Db 301 CTGGAAGGCTGGAGAGAACCAATTACCAACCTATATATCAAGAGCATGACAGAGAG 360  
QY 399 AATTGGTTTGTGGCTCAAGAGAAATGGAGCTGCAAAACGGGCTCTTAAACTCACTAT 458  
Db 361 AATTGGTTTGTGGCTCAAGAGAAATGGAGCTGCAAAACGGGCTCTTAAACTCACTAT 420  
QY 459 GGCAGAAAGCAATCTTCTTCCCTCCGACGCTCTCTGATTA 506  
Db 421 GGCAGAAAGCAATCTTCTTCCCTCCGACGCTCTCTGATTA 468

RESULT 8

US-10-649-480-3  
; Sequence 3, Application US/10649480  
; Publication No. US20040115769A1  
; GENERAL INFORMATION:  
; APPLICANT: Stegmann, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155  
; FILE REFERENCE: CVGENG.008A  
; CURRENT APPLICATION NUMBER: US/10/649,480  
; CURRENT FILING DATE: 2003-08-27  
; PRIOR APPLICATION NUMBER: 10/649,480  
; PRIOR FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-649-480-3

Query Match 72.6%; Score 463.2; DB 17; Length 468;  
Best Local Similarity 99.4%; Pred. No. 1e-145;  
Matches 465; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 39 ATGGCTGAAGGGGAAATCACCACCTTTCACAGCCCTGACGAGAGTTTAACTGCTCCA 98  
Db 1 ATGGCTGAAGGGGAAATCACCACCTTTCACAGCCCTGACGAGAGTTTAACTGCTCCA 60  
QY 99 GGGAAATTACAAAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCCACTTCTGAGATC 158  
Db 61 GGGAAATTACAAAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCCACTTCTGAGATC 120  
QY 159 CTTCCGGATGGCAGCAGTGGATGGGACAGGAGGACAGGAGGACACGACATTCAGCTGCAG 218  
Db 121 CTTCCGGATGGCAGCAGTGGATGGGACAGGAGGACAGGAGGACACGACATTCAGCTGCAG 180  
QY 219 CTCAGTGGGAAAGCGTGGGAGAGTGTATATAAGAGTACCGAGCTGCGGACTGCTAT 278  
Db 181 CTCAGTGGGAAAGCGTGGGAGAGTGTATATAAGAGTACCGAGCTGCGGACTGCTAT 240  
QY 279 GCATGGACACCGCAGCGGCTTTTATACGGCTTCACACACCAATGAGAAATGTTGTC 338  
Db 241 GCATGGACACCGCAGCGGCTTTTATACGGCTTCACACACCAATGAGAAATGTTGTC 300  
QY 339 CTGGAAGGCTGGAGAGAACCAATTACCAACCTATATATCAAGAGCATGACAGAGAG 398  
Db 301 CTGGAAGGCTGGAGAGAACCAATTACCAACCTATATATCAAGAGCATGACAGAGAG 360  
QY 399 AATTGGTTTGTGGCTCAAGAGAAATGGAGCTGCAAAACGGGCTCTTAAACTCACTAT 458  
Db 361 AATTGGTTTGTGGCTCAAGAGAAATGGAGCTGCAAAACGGGCTCTTAAACTCACTAT 420  
QY 459 GGCAGAAAGCAATCTTCTTCCCTCCGACGCTCTCTGATTA 506  
Db 421 GGCAGAAAGCAATCTTCTTCCCTCCGACGCTCTCTGATTA 468

RESULT 9  
US-09-929-918-1  
; Sequence 1, Application US/09929918  
; Patent No. US2002090678A1  
; GENERAL INFORMATION:  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF  
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES  
; FILE REFERENCE: PHAGE.006A  
; CURRENT APPLICATION NUMBER: US/09/929,918  
; CURRENT FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: 09/318,288  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 630  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: This sequence was chemically synthesized based  
; OTHER INFORMATION: upon the amino acid sequence of human acidic  
; OTHER INFORMATION: fibroblast growth factor (155 amino acids) using  
; OTHER INFORMATION: codons which are used in highly expressed proteins from E. coli.  
; NAME/KEY: CDS  
; LOCATION: (122)....(590)  
US-09-929-918-1

Query Match 49.2%; Score 314.2; DB 9; Length 630;  
Best Local Similarity 79.2%; Pred. No. 2.9e-95;  
Matches 373; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 39 ATGGCTGAAGGGGAAATCACCACCTTTCACAGCCCTGACGAGAGTTTAACTGCTCCA 98  
Db 122 ATGGCTGAAGGGGAAATCACCACCTTTCACAGCCCTTACCGGTTAAACGAGAAATTAACCTCCGCC 181  
QY 99 GGGAAATTACAAAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCCACTTCTGAGATC 158  
Db 182 GGGAAATTACAAAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCCACTTCTGAGATC 241  
QY 159 CTTCCGGATGGCAGCAGTGGATGGGACAGGAGGACAGGAGGACACGACATTCAGCTGCAG 218  
Db 121 CTTCCGGATGGCAGCAGTGGATGGGACAGGAGGACAGGAGGACACGACATTCAGCTGCAG 180

Db 242 CTGCGAGTGGGACAGTACATGGGAGCTGCGGATCGCTCCGACGACACATTCAGCTGCAA 301  
QY 219 CTCATGCGGAAAGCGTGGGGAGGTGTATATAAAGTACCGAGACTGGCGAGTACTTG 278  
Db 302 CTCTCGCGCGAAAGCGTGGAGAGTCTATATCAAGTCGACGGAGCTGGCGAGTACTT 361  
QY 279 GGCATGACACCGAGCGGCTTTTATACGGCTCAGACACCAAAATGAGAAATGTTGTTTC 338  
Db 362 GGCATGACACCGAGCGGCTTTTATACGGCTCAGACACCAAAATGAGAAATGTTGTTTC 338  
QY 339 CTGAAAAGGCTGGAGAGAACATTACAAACCTTATATCCAGAAAGCATGACAGAG 398  
Db 422 CTGAAAAGGCTGGAGAGAACATTACAAACCTTATATCCAGAAAGCATGACAGAG 481  
QY 399 AATTGCTTTGCTGGCTCAGAGAGATGGAGCTGCAAAAGCGGCTCTTAAACTCTACTAT 458  
Db 482 AACTGCTTTGAGGCTTTAAAGAAATGGTCTTGAAGCGTGGACCGACTGCTACTAT 541  
QY 459 GGCAGAAAGCAATCTTGTTCCTCCCTCCGAGTCTCTCTGATTAAAGA 509  
Db 542 GGCAGAAAGCAATCTTGTTCCTCCCTCCGAGTCTCTCTGATTAAAGA 592

RESULT 10

US-09-929-945-1

; Sequence 1, Application US/09929945  
; Patent No. US2002015532A1  
; GENERAL INFORMATION:  
; APPLICANT: Stegmann, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
; FILE REFERENCE: CVGENG.008A  
; CURRENT APPLICATION NUMBER: US/09/929,945  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 630  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized sequence for human acidic  
; OTHER INFORMATION: Fibroblast Growth Factor (155 amino acids) using  
; OTHER INFORMATION: preferred codons for E. coli  
; NAME/KEY: CDS  
; LOCATION: (122)...(590)  
US-09-929-945-1

Query Match 49.2%; Score 314.2; DB 9; Length 630;  
Best Local Similarity 79.2%; Pred. No. 2.9e-95;  
Matches 373; Conservative 0; Mismatches 98; Indels 0; Gaps 0;  
QY 39 ATGCTGAAGGGGAAATACCACTTTCAGAGCTGACCGAGAGTGTAACTTCGCTCCA 98  
Db 122 ATGCTGAAGGGGAAATACCACTTTCAGAGCTGACCGAGAGTGTAACTTCGCTCCA 181  
QY 99 GGGAAATTACAGAGCCCAAACTCTTACTGTAGCAAGCGGGGCCACTTCCTGAGGATC 158  
Db 182 GGGAAATTACAGAGCCCAAACTCTTACTGTAGCAAGCGGGGCCACTTCCTGAGGATC 241  
QY 159 CTTCGGATGGCAGTGGATGGGACAGGAGCGACACCAATTCAGCTGCAG 218  
Db 242 CTTCGGATGGCAGTGGATGGGACAGGAGCGACACCAATTCAGCTGCAG 301  
QY 219 CTCAGTGGGAAAGCGTGGGAGGTGTATATAAAGTACCGAGACTGGCGAGTACTTG 278  
Db 302 CTCTCGCGCGAAAGCGTGGAGAGTCTATATCAAGTCGACGGAGCTGGCGAGTACTT 361  
QY 279 GGCATGACACCGAGCGGCTTTTATACGGCTCAGACACCAAAATGAGAAATGTTGTTTC 338  
Db 362 GGCATGACACCGAGCGGCTTTTATACGGCTCAGACACCAAAATGAGAAATGTTGTTTC 338  
QY 339 CTGAAAAGGCTGGAGAGAACATTACAAACCTTATATCCAGAAAGCATGACAGAG 398  
Db 422 CTGAAAAGGCTGGAGAGAACATTACAAACCTTATATCCAGAAAGCATGACAGAG 481  
QY 399 AATTGCTTTGCTGGCTCAGAGAGATGGAGCTGCAAAAGCGGCTCTTAAACTCTACTAT 458  
Db 482 AACTGCTTTGAGGCTTTAAAGAAATGGTCTTGAAGCGTGGACCGACTGCTACTAT 541  
QY 459 GGCAGAAAGCAATCTTGTTCCTCCCTCCGAGTCTCTCTGATTAAAGA 509  
Db 542 GGCAGAAAGCAATCTTGTTCCTCCCTCCGAGTCTCTCTGATTAAAGA 592

QY 399 AATTGCTTTGCTGGCTCAGAGAGATGGAGCTGCAAAAGCGGCTCTTAAACTCTACTAT 458  
Db 482 AACTGCTTTGAGGCTTTAAAGAAATGGTCTTGAAGCGTGGACCGACTGCTACTAT 541  
QY 459 GGCAGAAAGCAATCTTGTTCCTCCCTCCGAGTCTCTCTGATTAAAGA 509  
Db 542 GGCAGAAAGCAATCTTGTTCCTCCCTCCGAGTCTCTCTGATTAAAGA 592

RESULT 11

US-10-280-864-1  
; Sequence 1, Application US/10280864  
; Publication No. US20030054492A1  
; GENERAL INFORMATION:  
; APPLICANT: Stegmann, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
; FILE REFERENCE: CVGENG.008A  
; CURRENT APPLICATION NUMBER: US/10/280,864  
; CURRENT FILING DATE: 2002-10-24  
; PRIOR APPLICATION NUMBER: US/09/929,945  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 630  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized sequence for human acidic  
; OTHER INFORMATION: Fibroblast Growth Factor (155 amino acids) using  
; OTHER INFORMATION: preferred codons for E. coli  
; NAME/KEY: CDS  
; LOCATION: (122)...(590)  
US-10-280-864-1

Query Match 49.2%; Score 314.2; DB 15; Length 630;  
Best Local Similarity 79.2%; Pred. No. 2.9e-95;  
Matches 373; Conservative 0; Mismatches 98; Indels 0; Gaps 0;  
QY 39 ATGCTGAAGGGGAAATACCACTTTCAGAGCTGACCGAGAGTGTAACTTCGCTCCA 98  
Db 122 ATGCTGAAGGGGAAATACCACTTTCAGAGCTGACCGAGAGTGTAACTTCGCTCCA 181  
QY 99 GGGAAATTACAGAGCCCAAACTCTTACTGTAGCAAGCGGGGCCACTTCCTGAGGATC 158  
Db 182 GGGAAATTACAGAGCCCAAACTCTTACTGTAGCAAGCGGGGCCACTTCCTGAGGATC 241  
QY 159 CTTCGGATGGCAGTGGATGGGACAGGAGCGACACCAATTCAGCTGCAG 218  
Db 242 CTTCGGATGGCAGTGGATGGGACAGGAGCGACACCAATTCAGCTGCAG 301  
QY 219 CTCAGTGGGAAAGCGTGGGAGGTGTATATAAAGTACCGAGACTGGCGAGTACTTG 278  
Db 302 CTCTCGCGCGAAAGCGTGGAGAGTCTATATCAAGTCGACGGAGCTGGCGAGTACTT 361  
QY 279 GGCATGACACCGAGCGGCTTTTATACGGCTCAGACACCAAAATGAGAAATGTTGTTTC 338  
Db 362 GGCATGACACCGAGCGGCTTTTATACGGCTCAGACACCAAAATGAGAAATGTTGTTTC 338  
QY 339 CTGAAAAGGCTGGAGAGAACATTACAAACCTTATATCCAGAAAGCATGACAGAG 398  
Db 422 CTGAAAAGGCTGGAGAGAACATTACAAACCTTATATCCAGAAAGCATGACAGAG 481  
QY 399 AATTGCTTTGCTGGCTCAGAGAGATGGAGCTGCAAAAGCGGCTCTTAAACTCTACTAT 458  
Db 482 AACTGCTTTGAGGCTTTAAAGAAATGGTCTTGAAGCGTGGACCGACTGCTACTAT 541  
QY 459 GGCAGAAAGCAATCTTGTTCCTCCCTCCGAGTCTCTCTGATTAAAGA 509  
Db 542 GGCAGAAAGCAATCTTGTTCCTCCCTCCGAGTCTCTCTGATTAAAGA 592

# RESULT 12

US-10-649-480-1

Sequence 1, Application US/10649480  
Publication No. US20040115769A1  
GENERAL INFORMATION:  
APPLICANT: Stegmann, Thomas  
APPLICANT: Kordyum, Vitaliy A.  
APPLICANT: Chernykh, Svitlana I.  
APPLICANT: Slavchenko, Iryna Yu.  
APPLICANT: Vozlanov, Oleksandr  
TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155  
FILE REFERENCE: CVGENG 008A  
CURRENT APPLICATION NUMBER: US/10/649,480  
PRIOR FILING DATE: 2003-08-27  
PRIOR APPLICATION NUMBER: 10/649,480  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 630  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chemically synthesized sequence for human acidic  
OTHER INFORMATION: Fibroblast Growth Factor (155 amino acids) using  
OTHER INFORMATION: preferred codons for E. coli  
NAME/KEY: CDS  
LOCATION: (122)...(590)  
US-10-649-480-1

Query Match 49.2%; Score 314.2; DB 17; Length 630;  
Best Local Similarity 79.2%; Pred. No. 2.9e-95;  
Matches 373; Conservative 0; Mismatches 98; Indels 0; Gaps 0;  
QY 39 ATGGCTGAGGGGAATCACCACCTTCACAGCCCTGACCGAGCTTTAATTCGCTCCA 98  
Db 122 ATGGCTGAGGGGAATCACCACCTTCACAGCCCTGACCGAGCTTTAATTCGCTCCA 181  
QY 99 GGGAAATTACAGAGCCAAATCTCTTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 158  
Db 182 GGGAAATTACAGAGCCAAATCTCTTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 241  
QY 159 CTTCGGATGCGACAGTGGATGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 218  
Db 242 CTTCGGATGCGACAGTGGATGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 301  
QY 219 CTCAGTGGCAAGAGCGTGGGGAGAGTGTATATAAGAGTACCGAGCTGGCCAGTCTTG 278  
Db 302 CTCCTGGCCGAAAGCGTGGAGAGTGTATATAAGAGTACCGAGCTGGCCAGTCTTG 361  
QY 279 GCGATGACACCGAGCGGCTTTTATACGGCTCAGACACCAATAGAGGAGTGTGTTTC 338  
Db 362 GCGATGACACCGAGCGGCTTTTATACGGCTCAGACACCAATAGAGGAGTGTGTTTC 421  
QY 339 CTGGAAGGCTGGAGGAGAACCTTACACACCTATATATCCAGAGAGATCGAGAGAG 398  
Db 422 CTGGAAGGCTGGAGGAGAACCTTACACACCTATATATCCAGAGAGATCGAGAGAG 481  
QY 399 AATTGGTTTGTGGCTCAAGAGATGGAGCTGCAACCGGGCTCTTAAACTCACTAT 458  
Db 482 AACTGGTTTGTAGGCTTAAAGGCTTAAAGGCTTAAAGGCTTAAAGGCTTAAAGGCT 541  
QY 459 GCGCAGAGCAATCTTGTCTTCCCTGCGAGCTCTTCTTGATTAAAGA 509  
Db 542 GCGCAGAGCAATCTTGTCTTCCCTGCGAGCTCTTCTTGATTAAAGA 592

# RESULT 13

US-09-929-918-10  
Sequence 10, Application US/09929918  
Patent No. US20020090678A1  
GENERAL INFORMATION:  
APPLICANT: Kordyum, Vitaliy A.  
APPLICANT: Chernykh, Svitlana I.  
APPLICANT: Slavchenko, Iryna Yu.  
APPLICANT: Vozlanov, Oleksandr  
TITLE OF INVENTION: PHASE-DEPENDENT SUPER PRODUCTION OF

TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES  
FILE REFERENCE: PHAGE.006A  
CURRENT APPLICATION NUMBER: US/09/929,918  
CURRENT FILING DATE: 2001-08-15  
PRIOR APPLICATION NUMBER: 09/318,288  
PRIOR FILING DATE: 1999-05-25  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 10  
LENGTH: 990  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chemically synthesized sequence for human  
OTHER INFORMATION: interferon alpha-2b  
NAME/KEY: Promoter  
LOCATION: (231)...(249)  
NAME/KEY: CDS  
LOCATION: (320)...(784)  
US-09-929-918-10

Query Match 49.2%; Score 314.2; DB 9; Length 990;  
Best Local Similarity 79.2%; Pred. No. 3.6e-95;  
Matches 373; Conservative 0; Mismatches 98; Indels 0; Gaps 0;  
QY 39 ATGGCTGAGGGGAATCACCACCTTCACAGCCCTGACCGAGGAGTGTAAATTCGCTCCA 98  
Db 320 ATGGCTGAGGGGAATCACCACCTTCACAGCCCTGACCGAGGAGTGTAAATTCGCTCCA 379  
QY 99 GCGAATTACAGAGCCAAATCTCTTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 158  
Db 380 GCGAATTACAGAGCCAAATCTCTTACTGTAGCAACGGGGGCCACTTCCTGAGGATC 439  
QY 159 CTTCGGATGCGACAGTGGATGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 218  
Db 440 CTTCGGATGCGACAGTGGATGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 499  
QY 219 CTCAGTGGCAAGAGCGTGGGGAGAGTGTATATAAGAGTACCGAGCTGGCCAGTCTTG 278  
Db 500 CTCCTGGCCGAAAGCGTGGAGAGTGTATATAAGAGTACCGAGCTGGCCAGTCTTG 559  
QY 279 GCGATGACACCGAGCGGCTTTTATACGGCTCAGACACCAATAGAGGAGTGTGTTTC 338  
Db 560 GCGATGACACCGAGCGGCTTTTATACGGCTCAGACACCAATAGAGGAGTGTGTTTC 619  
QY 339 CTGGAAGGCTGGAGGAGAACCTTACACACCTATATATCCAGAGAGATCGAGAGAG 398  
Db 620 CTGGAAGGCTGGAGGAGAACCTTACACACCTATATATCCAGAGAGATCGAGAGAG 679  
QY 399 AATTGGTTTGTGGCTCAAGAGATGGAGCTGCAACCGGGCTCTTAAACTCACTAT 458  
Db 680 AACTGGTTTGTAGGCTTAAAGGCTTAAAGGCTTAAAGGCTTAAAGGCTTAAAGGCT 739  
QY 459 GCGCAGAGCAATCTTGTCTTCCCTGCGAGCTCTTCTTGATTAAAGA 509  
Db 740 GCGCAGAGCAATCTTGTCTTCCCTGCGAGCTCTTCTTGATTAAAGA 790

# RESULT 14

US-09-968-007A-133  
Sequence 133, Application US/09968007A  
Publication No. US20040115625A1  
GENERAL INFORMATION:  
APPLICANT: Emer, Reinhard  
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature  
FILE REFERENCE: Gene Sets  
FILE REFERENCE: 689290-71  
CURRENT APPLICATION NUMBER: US/09/968,007A  
CURRENT FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: US/60/237,172  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,173  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,278  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,294  
PRIOR FILING DATE: 2000-10-02  
PRIOR APPLICATION NUMBER: US/60/237,295  
PRIOR FILING DATE: 2000-10-02

; PRIOR APPLICATION NUMBER: US/60/237,316  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 1001  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 133  
; LENGTH: 3658  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-968-007A-133

Query Match 47.5%; Score 302.8; DB 12; Length 3658;  
Best Local Similarity 96.0%; Pred. No. 4.8e-91;  
Matches 332; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 294 GGGCTTTTATACGGCTCAGACACCAATGAGGAATGTTGTTCTGGAAGGCTGGAG 353  
Db GTGGTTTATCTTTTAGCAGACCAATGAGGAATGTTGTTCTGGAAGGCTGGAG 345

QY 354 GAGACCAATTACCAACCTATATATCCAGAGCATGCAAGAGAAATGTTGTTGGC 413  
Db GAGAACCATTACCAACCTATATATCCAGAGCATGCAAGAGAAATGTTGTTGGC 405

QY 414 CTCAGAGAAATGCGAGCTGCAAAACGGCTCTAAACTCACTATGCGCAGAAAGCAATC 473  
Db CTCAGAGAAATGCGAGCTGCAAAACGGCTCTAAACTCACTATGCGCAGAAAGCAATC 465

QY 474 TTGTTTCTCCCTCCAGTCTCTCTGATTAAGAGATCTGTCT-GGTGTTGACCACT 532  
Db TTGTTTCTCCCTCCAGTCTCTCTGATTAAGAGATCTGTCTGCGGTGTTGACCACT 525

QY 533 CCAGAGAGTTTCGAGGGTCTCACTGTTGACCCCAAAAATGTTCCCTTGACCAATG 592  
Db CCAGAGAGTTTCGAGGGTCTCACTGTTGACCCCAAAAATGTTCCCTTGACCAATG 584

QY 593 GCTGCGCTAACCCCGAGCCGAGCCCTGGAATTTGTAAGCAACTT 638  
Db GCTGCGCTAACCCCGAGCCGAGCCCTGGAATTTGTAAGCAACTT 630

RESULT 15

US-09-968-007A-440  
; Sequence 440, Application US/09968007A  
; Publication No. US20040115625A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner, Reinhard  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature  
; FILE OF INVENTION: Gene Sets  
; FILE REFERENCE: 689290-71  
; CURRENT APPLICATION NUMBER: US/09/968,007A  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,172  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,173  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,278  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,294  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,295  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,316  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 1001  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 440  
; LENGTH: 3658  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-968-007A-440

Query Match 47.5%; Score 302.8; DB 12; Length 3658;  
Best Local Similarity 96.0%; Pred. No. 4.8e-91;  
Matches 332; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

QY 294 GGGCTTTTATACGGCTCAGACACCAATGAGGAATGTTGTTCTGGAAGGCTGGAG 353  
Db GTGGTTTATCTTTTAGCAGACCAATGAGGAATGTTGTTCTGGAAGGCTGGAG 345

QY 354 GAGACCAATTACCAACCTATATATCCAGAGCATGCAAGAGAAATGTTGTTGGC 413  
Db GAGAACCATTACCAACCTATATATCCAGAGCATGCAAGAGAAATGTTGTTGGC 405

Db 346 GAGACCAATTACCAACCTATATATCCAGAGCATGCAAGAGAAATGTTGTTGGC 405  
QY 414 CTCAGAGAAATGCGAGCTGCAAAACGGCTCTAAACTCACTATGCGCAGAAAGCAATC 473  
Db CTCAGAGAAATGCGAGCTGCAAAACGGCTCTCGGACTCACTATGCGCAGAAAGCAATC 465

QY 474 TTGTTTCTCCCTCCAGTCTCTCTGATTAAGAGATCTGTCT-GGTGTTGACCACT 532  
Db TTGTTTCTCCCTCCAGTCTCTCTGATTAAGAGATCTGTCTGCGGTGTTGACCACT 525

QY 533 CCAGAGAGTTTCGAGGGTCTCTCACTGTTGACCCCAAAAATGTTCCCTTGACCAATG 592  
Db CCAGAGAGTTTCGAGGGTCTCTCACTGTTGACCCCAAAAATGTTCCCTTGACCAATG 584

QY 593 GCTGCGCTAACCCCGAGCCGAGCCCTGGAATTTGTAAGCAACTT 638  
Db GCTGCGCTAACCCCGAGCCGAGCCCTGGAATTTGTAAGCAACTT 630

Search completed: August 24, 2004, 21:00:18  
Job time : 484 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 18:35:10 ; Search time 2845 Seconds  
(without alignments)  
6696.686 Million cell updates/sec

Title: US-10-022-554A-3  
Perfect score: 638  
Sequence: 1 gaattcggaacgcgcaca.....cctgaattgtaagcaactt 638

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estm.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pin.\*  
20: em\_gss\_vit.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rod.\*  
26: em\_gss\_pig.\*  
27: em\_gss\_vit.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	%	
1	601.8	94.3	1173	13	BX444567	BX444567 BX444567		
2	576.8	90.4	832	12	B1869731	B1869731 603393620		
3	569.4	89.2	1057	13	BQ067949	BQ067949 AGENCOURT		
4	567	88.9	1084	12	BM809005	BM809005 AGENCOURT		
5	560.8	87.9	878	12	B1753845	B1753845 603027526		
6	555.8	87.7	821	12	B1598390	B1598390 603250094		
7	511.4	80.2	534	9	A1590078	A1590078 tme8c01.x		
8	501.6	78.6	714	12	BG706412	BG706412 602669744		
9	437.6	68.6	472	9	A1077609	A1077609 oy26d02.s		
10	434.6	68.1	3404	11	AK035330	AK035330 Mus muscu		
11	425.4	66.7	843	12	B1692283	B1692283 603342751		
12	424.2	66.5	461	10	BF956865	BF956865 RCL-NN023		
13	420.6	65.9	2206	11	BC027001	BC027001 Mus muscu		
14	408.2	64.0	663	9	A1119291	A1119291 ue95c07.y		
15	404	63.3	855	12	B1313990	B1313990 602984393		
16	402.2	63.0	750	13	BUC27243	BUC27243 U1-H-FGC-		
17	401.2	62.9	508	29	CG533840	CG533840 OGT153987		
18	385.4	60.4	526	29	CG565930	CG565930 OGT191133		
19	385.2	60.4	631	10	BB627624	BB627624 B8627624		
20	385.2	60.4	689	9	A1663400	A1663400 uk32d07.y		
21	356	55.6	813	10	BF532970	BF532970 602073491		
22	354.6	55.6	611	13	BU840197	BU840197 AGENCOURT		
23	338.6	51.5	386	10	BF958824	BF958824 CM3-NN024		
24	337.4	51.3	503	10	BF442355	BF442355 259038 MA		
25	323.6	50.3	747	485	29	CG554707	CG554707 OST168594	
26	320.6	50.3	522	14	CD701495	CD701495 EST18019		
27	316.8	49.7	529	29	CG629018	CG629018 OST340697		
28	316.6	49.6	543	9	AA261582	AA261582 tme87c09.r		
29	307.8	48.2	395	14	CB773841	CB773841 AGENCUC:S		
30	302	47.3	701	12	BM995210	BM995210 U1-H-ED0-		
31	298.8	46.8	469	10	AW259195	AW259195 B839f09.y		
32	292.2	45.8	570	12	BM364189	BM364189 SM3000090		
33	291.4	45.7	570	12	B1598882	B1598882 603247981		
34	281	44.0	458	9	AA594274	AA594274 nl190g01.s		
35	280.6	44.0	420	13	KA488304	KA488304 DKP2686G		
36	279	43.7	415	9	A1083919	A1083919 qf26c07.x		
37	274.2	43.0	458	14	R54255	R54255 Y974f06.r1		
38	274	42.9	460	9	AA015793	AA015793 xz30a12.r		
39	273.6	42.9	424	14	H23109	H23109 ymc3f12.r1		
40	267.4	41.9	384	9	AA238828	AA238828 tme92h02.r		
41	262.8	41.2	642	10	B8629001	B8629001 BB629001		
42	261.8	41.0	429	10	B531286	B531286 U1-R-C4-a		
43	251.8	39.5	403	29	CG613113	CG613113 OST7299916		
44	247	38.7	436	10	B8850804	B8850804 B8450804		
45	246	38.6	309	29	CG496943	CG496943 OST73278		

## ALIGNMENTS

[illegible]

Genoscope - Centre National de Sequençage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Library was constructed by life technologies, a division of  
Invitrogen. This sequence belongs to sequence cluster 3201.r For  
more information about this cluster, see  
<http://www.genoscope.cns.fr/>  
cgi-bin/cluster.cgi?seq=CSD0N003DH080P1&cluster=3201.r. Contact :  
Peng Liang Email : [liang@lifetech.com](mailto:liang@lifetech.com) URL :  
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600  
Faraday Avenue Genoscope sequence ID : CSD0N003DH080P1.

## FEATURES

```

1. .l173
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN003YP16"
/tissue_type="ADULT BRAIN"
/dev stage="adult"

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(clone\_lib="Homo sapiens ADULT BRAIN"  
note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA  
was primed with a NotI-oligo(dT) primer. Five prime end  
enriched, double-strand cDNA was digested with NotI and  
cloned into the NotI and EcoRV sites of the pCMVSPORT 6  
vector. Library was not normalized."

## ORIGIN

Query Match            94.3%;     Score 601.8;   DB 13;   Length 1173;  
Best Local Similarity   98.6%;     Pred. No. 6.9e-166;  
Matches 528: Concentrating        0

3	ATTGGGAACGGCCAAAGCAGCAGCTCTGAGCCATGCGTGAAGGGGAATCAACACC	62
Db		
132	AGTCTTTGAAGCGCCAAAGCAGCAGCTCTGAGCCATGCGTGAAGGGGAATCAACACC	191
QY		
63	TTACAGCCCTGACCCGAGAAGTTTAAATCTGCTCCAGGGAATACAGAGAGCCCAACTC	122
Db		
192	TTACAGCCCTGACCCGAGAGTGTATATCTGCTCCAGGGAATACAGAGAGCCCAACTC	251
QY		
123	CTCTACTGTAGCAACGGGGGCCATCTTCTGAGATCTTTCGGATGGCACTGATGGG	182
Db		
252	CTCTACTGTAGCAACGGGGGCCATCTTCTGAGATCTTTCGGATGGCACTGATGGG	311
QY		
183	ACAAGGGAAGGCGAGCCAGCACATCTACAGCTGCGACTCAGTGGCGAAGCGTGGGGAG	242
Db		
312	ACAAGGGAAGGCGAGCCAGCACATCTACAGCTGCGACTCAGTGGCGAAGCGTGGGGAG	371
QY		
243	GTGTATATAAGAGTACCAGAGCTGGCCAGTACTTGGCCATGTGACACCGACGGGCTTTA	302
Db		
372	GTGTATATAAGAGTACCAGAGCTGGCCAGTACTTGGCCATGTGACACCGACGGGCTTTA	431
QY		
303	TAGCGCTCAGACACCAAAATGAGAAATGTTTGTCTCGAAAGGCTGGAGAGAACCAT	362
Db		
432	TAGCGCTCAGACACCAAAATGAGAAATGTTTGTCTCGAAAGGCTGGAGAGAACCAT	491
QY		
363	TACAACCTATATATCCAAGAGACATCGACAGAGAAATGGTTTGTGGCCTCAGAGAG	422
Db		
492	TACAACCTATATATCCAAGAGACATCGACAGAGAAATGGTTTGTGGCCTCAGAGAG	551
QY		
423	AATGGAGCTGCAAGCGGTCTTAAACTCATATGTCAGAAAGCAACTTGTGTTCTC	482
Db		
552	AATGGAGCTGCAAGCGGTCTCTCGAAGTCTATGTCAGAAAGCAACTTGTGTTCTC	611
QY		
483	CCCTGGCCAGTCTCTTCGATTAAGAGATCTGTCTTCTGGTGTGACCATCTCAGAGAG	541
Db		
612	CCCTGGCCAGTCTCTTCGATTAAGAGATCTGTCTTCTGGTGTGACCATCTCAGAGAG	671
QY		
542	TTTTCAGGGGTCTCAGCTGGTTGACCCCAAAAATGTTTCCTTGACCAATGGCTCGGCTA	601
Db		
672	TTTTCAGGGGTCTCAGCTGGTTGACCCCAAAAATGTTTCCTTGACCAATGGCTCGGCTA	730
QY		
602	ACCCCGAGCCACAGAGCGCTGAATTTGTAGCAACTT	638
Db		
731	ACCCCGAGCCACAGAGCGCTGAATTTGTAGCAACTT	767

## RESULT 2

BI869731

LOCUS

BI869731	832 bp	mRNA	linear	EST 11-OCT-2001
----------	--------	------	--------	-----------------



DEFINITION	603393620Fl NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5403677 5', mRNA sequence.
ACCESSION	U869731
VERSION	U869731.1 GI:16043404
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	1. (bases 1 to 832) Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: c9apbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

source	1..832
Location/Qualifiers	
High quality sequence stop:	829.
Plate:	LLAM12029
row:	9
column:	06
http://image.llnl.gov	

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/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="IMAGE:5403677"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 90"
/notes="Organ: liver; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."

```

Query Match	90.4%;	Score 576.8;	DB 12;	Length 832;
Best local Similarity	98.3%;	Pred. No. 1.4e-158;		
Matches 625;	Conservative	0;	Mismatches 7;	Indels 4;
			Gaps	4

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106 CACAGCCCTGACCGAGAGATTAACTCCCGGGAATACAGAGGCCCAACTCTCT 165  
125 CTACTGTAGCAACGGGGCCACTTCTCTCAGGATCTCTCCGGATGCCACAGTGGATGGGAC 184

166 CTACTGTAGCAACGGGGGCCATCTCTCGAGTCTTCCGATCGCACAGTGGATGGCAC 225

185 AAGGGACAGAGCGCACCGACATTCAGCTGCAGCTCAGTSCGGAAGCGTGGGGNGGT 244

226 AAGGGACAGAGCGCACCGACATTCAGCTGCAGCTCAGTSCGGAAGCGTGGGGNGGT 285

245 GTATATAAGAGTACCGAGACTGCGCAGTACTTGGCGATGACACCGAGCGGCTTTTATA 304  
286 GTATATTAAGAGTACCGAGACTGCGCGAGTACTTGGCCATGACACCGAGCGGCTTTTATA 345  
305 CGGCTACACAGACACCAATGAGAGATGTTGTCTCGAAAGCGCTGAGAGAGACCACTTA 364

[illegible]

425 TGGGAGCTGCAAA-CCGGGTCTCTAAAACCTCACTATGCGCAGAAAGCAATCTGTGTTCTCC 483  
|||||  
465 TGGGAGCTGCAAAACCGGTCTCTCGGACTCACTATGCGCAGAAAGCAATCTGTGTTCTCC 524  
|||||

484 CCTGCCAGTCTCTTCTGATTAAAGAGATCTGTCT - GGTGTGACCACTCCAGAGAAGT 542  
|||||  
525 CCTGCCAGTCTCTTCTGATTAAAGAGATCTGTCTGGGTAGACCACTCCAGAGAAGT 584

---







# RESULT 7

AI590078/c  
LOCUS  
DEFINITION  
tm58c01.x1 NCI CGAP Brn25 Homo sapiens cDNA clone IMAGE:2162304 3', similar to gb:U3361 HEPARIN-BINDING GROWTH FACTOR PRECURSOR 1 (HUMAN); mRNA sequence.

AI590078  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AI590078.1 GI:4599126  
EST.  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 534)  
NCI/NINDS-GAP http://www.ncbi.nlm.nih.gov/hcicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTCAP), Tumor Gene Index

Unpublished (1998)  
JOURNAL

Contact: Robert Strausberg, Ph.D.  
COMMENT

Email: c9apbs-r@mail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html  
Insert length: 736 Std Error: 0.00

Seq primer: -40UP from Gibco  
High quality sequence stop: 455.

Location/Qualifiers

1..534

/organism="Homo sapiens"

/mol\_type="mRNA"

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/clone="IMAGE:2162304"

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/lab\_host="DH10B"

/clone.lib="NCI CGAP Brn25"

/note="Organ: brain; Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACCACTGAGTGGGCGCGCGCATAGGTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T3 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo."

## FEATURES

source  
Location/Qualifiers  
1..534  
High quality sequence stop: 710.

Query Match 80.2%; Score 511.4; DB 9; Length 534;  
Best Local Similarity 98.7%; Pred. No. 2.1e-139;  
Matches 526; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

9 GAAGCGCCACAGCAGCAGCTGCTGAGCCATGCTGAGGGGAAATACCACTTCACA 68  
|||||

534 GAAGCGCCACAGCAGCAGCTGCTGAGCCATGCTGAGGGGAAATACCACTTCACA 475  
|||||

69 GCCCTGACGAGAGGTTAATCTGCTCCAGGGAATTACAAGAGCCCAACTCTCTAC 128  
|||||

474 GCCCTGACGAGAGGTTAATCTGCTCCAGGGAATTACAAGAGCCCAACTCTCTAC 415  
|||||

129 TGTAGCAAGCGGGGCCACTCTCTGAGATCTTCGGATGCGCAGTGGAGCAAGG 188  
|||||

414 TGTAGCAAGCGGGGCCACTCTCTGAGATCTTCGGATGCGCAGTGGAGCAAGG 355  
|||||

189 GACAGAGGACCAACGACATTCAGTGTGAGTGTGAGTGTGAGTGTGAT 248  
|||||

354 GACAGAGGACCAACGACATTCAGTGTGAGTGTGAGTGTGAGTGTGAT 295  
|||||

249 ATAAGAGTACCGAGCTGCGCAGTGTGAGTGTGAGTGTGAGTGTGAT 308  
|||||

294 ATAAGAGTACCGAGCTGCGCAGTGTGAGTGTGAGTGTGAGTGTGAT 235  
|||||

309 TCACAGACCAATAGAGGAATGTGTGTTCTTGGAAAGGCTGGAGAGCAACATACAC 368  
|||||

Db 234 TCACAGACCAATAGAGGAATGTGTGTTCTTGGAAAGGCTGGAGAGCAACATACAC 175  
Qy 369 ACCTATATATCAAGAGCATGACAGAAAGTGTGTGTGCTTCAAGAAAGTGG 428  
Db 174 ACCTATATATCAAGAGCATGACAGAAAGTGTGTGTGCTTCAAGAAAGTGG 115  
Qy 429 AGCTCAAAACGGCTCTTAAACCTCATGTCGACAGAAAGTGTGTGTGCTTCAAGAAAGTGG 488  
Db 114 AGCTCAAAACGGCTCTTAAACCTCATGTCGACAGAAAGTGTGTGTGCTTCAAGAAAGTGG 55  
Qy 489 CCAGTCTCTTCTGATTAAGAGATCTGTCT-OGTGTGACCACTCCAGAGAA 540  
Db 54 CCAGTCTCTTCTGATTAAGAGATCTGTCTGCGGTGTGACCACTCCAGAGAA 2

RESULT 8  
Bg706412  
LOCUS

DEFINITION  
602669744P1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:4792378 5', mRNA sequence.

ACCESSION  
VERSION

Bg706412.1 GI:13981735  
EST.

KEYWORDS  
SOURCE

Homo sapiens (human)  
ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgi.nci.nih.gov/

1 (bases 1 to 714)  
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)  
JOURNAL

Contact: Robert Strausberg, Ph.D.  
COMMENT

Email: c9apbs-r@mail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10670 row: h column: 11  
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Location/Qualifiers

1..714

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/tissue\_type="hypothalamus"

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/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS-); Site\_1: BamHI; Site\_2: SalI-XhoI (9t-cgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTT-3', size-selected for average insert size 2.3 kb and normalized to 10^5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

Query Match 78.6%; Score 501.6; DB 12; Length 714;  
Best Local Similarity 96.5%; Pred. No. 1.9e-136;  
Matches 577; Conservative 0; Mismatches 14; Indels 7; Gaps 6;

Qy 3 ATTGGGAACCGCCACAGCAGCTGCTGAGCCATGCTGAGGGGAATACCAACC 62  
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114 AGCTTGAAGCGCCACAGCAGCTGCTGAGCCATGCTGAGGGGAATACCAACC 173  
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63 TTACAGCCCTGACCGAGAGTTTAAATCTGCTCCAGGGAAATTACAAGAGCCCAACTC 122  
|||||

174 TTACAGCCCTGACCGAGAGTTTAAATCTGCTCCAGGGAAATTACAAGAGCCCAACTC 232  
|||||

123 CTCTACTCTAGCAACGGGGGCACTCTCTGAGGATCTCTCGGATGGCAAGTGGATGG 182  
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233 CTCTACTCTAGCAACGGGGGCACTCTCTGAGGATCTCTCGGATGGCAAGTGGATGG 292  
|||||

## ORIGIN

183 ACAAGGACAGAGGACGACACATTCAGCTGACGCTCAGTCCGGAAGCGTGGGAG 242  
|||||  
293 ACAAGGACAGAGGACGACACATTCAGCTGACGCTCAGTCCGGAAGCGTGGGAG 352  
|||||  
243 GTGTATATAAGAGTACGAGACTGCGACATCTTGGCCATGACACCGAGCGGCTTTTA 302  
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353 GTGTATATAAGAGTACGAGACTGCGACATCTTGGCCATGACACCGAGCGGCTTTTA 412  
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303 TACGCTCAGACAGACACCAATAGGATGTTTCTTGGAAAGCGTGGAGGAGAACAT 362  
|||||  
413 TACGCTCAGACAGACACCAATAGGATGTTTCTTGGAAAGCGTGGAGGAGAACAT 472  
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363 TACACACCTATATATTCAGAGAGCTGCGAGAGAAATTTGTTTGGCTTCAAGAG 422  
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473 TACACACCTATATATTCAGAGAGCTGCGAGAGAAATTTGTTTGGCTTCAAGAG 532  
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423 AATGGAGCTGCAAAACCGGCTCTTAAACTCACTATGCGCAAGAGCAATCTTGTCT- 481  
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533 AATGGAGCTGCAAAACCGGCTCTTAAACTCACTATGCGCAAGAGCAATCTTGTCT 592  
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482 CCCCTCCAGCTCTCTTCTGATTA-AGAGATCTGTCTT-GGTGTTCACACTTCCAGAG 539  
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593 CCCCTCCAGCTCTCTTCTGATTA-AGAGATCTGTCTTGGTGTTCACACTTCCAGAG 652  
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540 AGTTTCAGAGGCTCTCTCACTGCTGTTGACCCCAAAAGTTCCTTGGCAATTTGGCTGC 597  
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LOCUS oy26d02.s1 Soares senescent fibroblasts NBHSP Homo sapiens cDNA  
clone IMAGE:1666947 3, similar to gb:MI3361 HEPARIN-BINDING GROWTH  
FACTOR PRECURSOR 1 (HUMAN);, mRNA sequence.  
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VERSION AI077609.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1. Soares et al. (1997)  
AUTHORS Soares, R., et al.  
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
JOURNAL NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicap.  
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Insert Length: 649 Std Error: 0.00  
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High quality sequence stop: 1.  
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/clone="IMAGE:1666947"  
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/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares senescent fibroblasts NBHSP"  
/notes="Vector: pT73D (Pharmacia) with a modified  
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RI; 1st strand cDNA was primed with a Not I - oligo(dT)  
primer [5']  
TGTTACCAATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTT 31,  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73D vector  
(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fatima Bonaldo."

Best Local Similarity 96.8%; Pred. NO. 1.1e-117;  
Matches 457; Conservative 0; Mismatches 14; Indels 1; Gaps 1;  
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|||||  
DB 472 AGCCCTCAGCAGAGGCTTAAATCTGCTCCAGGGAATTTACAAGAGCCCAACTCTCTTA 413  
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QY 128 CTGTAGCAAGGGGGGCGCACTTCTCAGAGATCTTCCGATCTTCCGATGCGCAGTGGATGGAACAAG 187  
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DB 412 CTGTAGCAAGGGGGGCGCACTTCTCAGAGATCTTCCGATGCGCAGTGGATGGAACAAG 353  
|||||  
QY 188 GGACAGGAGCGACACAGCAATTCAGCTGAGCTCAGTCCGGAAGCGTGGGAGAGTGTGA 247  
|||||  
DB 352 GGACAGGAGCGACACAGCAATTCAGCTGAGCTCAGTCCGGAAGCGTGGGAGAGTGTGA 293  
|||||  
QY 248 TATAAAGAGTACCGAGACTGCGACATCTTGGCCATGGAACCGACGCGCTTTTATACGG 307  
|||||  
DB 292 TATAAAGAGTACCGAGACTGCGACATCTTGGCCATGGAACCGACGCGCTTTTATACGG 233  
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QY 308 CTCACAGACCAAAATAGGAAATGTTTCTTCTGGAAGGCTGGAGGAGAACCTTACAA 367  
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DB 232 CTCACAGACCAAAATAGGAAATGTTTCTTCTGGAAGGCTGGAGGAGAACCTTACAA 173  
|||||  
QY 368 CACCTATATATTCAGAGAGCTGCGAGAGAAATTTGTTTGGCTTCAAGAGAAATGG 427  
|||||  
DB 172 CACCTATATATTCAGAGAGCTGCGAGAGAAATTTGTTTGGCTTCAAGAGAAATGG 113  
|||||  
QY 428 GAGCTGCAAAACCGGCTCTTAAACTCACTATGCGCAAGAGCAATCTTGTCTCCCGCT 487  
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DB 112 GAGCTGCAAAACCGGCTCTTAAACTCACTATGCGCAAGAGCAATCTTGTCTCCCGCT 53  
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QY 488 GCCAGTCTCTTCTGATTAAGAGATCTGTCTT-GGTGTTCACACTTCCAGAG 538  
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DB 52 GCCAGTCTCTTCTGATTAAGAGATCTGTCTTGGTGTTCACACTTCCAGAG 1  
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AK035330 3404 bp mRNA linear HTC 18-SEP-2003  
LOCUS AK035330  
DEFINITION Mus musculus adult male urinary bladder cDNA, RIKEN full-length  
enriched library, clone:9530018E22 product:fibroblast growth factor  
1, full insert sequence.  
ACCESSION AK035330.1 GI:26330609  
VERSION AK035330.1  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1. Carninci, P. and Hayashizaki, Y.  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
REFERENCE 2. Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159  
REFERENCE 3. Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Ozawa, Y., Izawa, M., Ohara, E., Matakaki, M.,  
Yoneda, Y., Ishikawa, T., Tanaka, K., Tanaka, T., Matsura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861  
REFERENCE 4. The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.

**FUNCTIONAL ANNOTATION OF A FULL-LENGTH MOUSE CDNA COLLECTION**  
 Nature 409, 685-690 (2001)  
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 (bases 1 to 3404)  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanaoka, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishii, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Shibata, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tagami, M., Tanaka, A., Takahashi, F., Takaku, Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission  
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome-gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
 CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome-gsc.riken.go.jp/  
 URL: http://fantom.gsc.riken.go.jp/

**FEATURES**  
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 Location/Qualifiers  
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 /db\_xref="MGI:2359577"  
 /db\_xref="taxon:10090"  
 /clone="9530018E22"  
 /sex="male"  
 /tissue type="urinary bladder"  
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 /translation="MAGEIT1PFLNPLNGYKPKLLVCSNGHFRILPDG  
 TVDGRSDIOHICOLDSSESGEYIKGTGQLAMDREGLYSGTQNECLFILE  
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**CDs**  
 Query Match 68.1%; Score 434.6; DB 11; Length 3404;  
 Best Local Similarity 84.3%; Pred. No. 2.5e-116;  
 Matches 512; Conservative 0; Mismatches 69; Indels 26; Gaps 1;

**ORIGIN**  
 28 GCTGCTGAGCCATGCTGAGAGGAGGAGATACACCTTACAGCCCTGACGAGAGTTTA 87  
 178 GCTGCGGAGCCATGCTGAGAGGAGGAGATACACCTTACAGCCCTGACGAGAGTTTA 237  
 88 ATCTGCTTCCAGGGAATACAGAGCCCAACCTCTCTTCTAGTACAGCCGAGGCTACT 147  
 238 ACCTGCTCTAGGAATACAGAGCCCAACCTCTCTTCTAGTACAGCCGAGGCTACT 297  
 148 TCTGAGATCTCTGAGTGGACAGAGTGGATGGAGGAGGAGGAGGAGGAGGAGGAGG 207  
 298 TCTTGGATCTCTTCTGATGGACCGTGGATGGAGGAGGAGGAGGAGGAGGAGGAGG 357

208 TTACGCTGAGCTCAGTGGCGAAGGCTGGGGAGGTGTATATAAGAGTACGAGACTG 267  
 358 TTACGCTGAGCTCAGTGGCGAAGGCTGGGGAGGTGTATATAAGAGTACGAGACTG 417  
 268 GCCAGTACTTGGCCATGGACACCGAGCGCTTTTATACGGCTCAGACACACCAATGAGG 327  
 418 GCCAGTACTTGGCCATGGACACCGAGCGCTTTTATACGGCTCAGACACCAATGAGG 477  
 328 AATGTTGCTGCTGGAAGGCTGGAGGAGACATTTACACACCTTATATCCAGAAGC 387  
 478 AATGTTGCTGCTGGAAGGCTGGAGGAGACATTTATTAACCTTACACCTTCCCAAGAGC 537  
 388 ATCCAGAGAGAAATTTGGTTTGTGGCTTCAAGAGAAATGGAGCTCCAAAGCGGCTCTA 447  
 538 ATCCAGAGAGAAATTTGGTTTGTGGCTTCAAGAGAAATGGAGCTTGAAGCGGCTCTC 597  
 448 AATCTCATATGCGCAGAGAAATTTGGTTTGTGGCTTCAAGAGAAATGGAGCTTGAAG 507  
 598 GAGTCTCATATGCGCAGAGAAATTTGGTTTGTGGCTTCAAGAGAAATGGAGCTTGAAG 657  
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 658 GAGTCTCATATGCGCAGAGAAATTTGGTTTGTGGCTTCAAGAGAAATGGAGCTTGAAG 691  
 568 CCCAAATATTTCTTACCATTTGGCTGCGCTTACCCCGCCAGCCAGAGCCCTGAATTT 627  
 692 CCTTACCATTTCTTACCATTTGGCTGCGCTTACCCCGCCAGCCAGAGCCCTGAATTT 751  
 628 GTAAGCA 634  
 752 GTAAGCA 758

**RESULT 11**  
 BI692283 843 bp mRNA linear EST 18-SEP-2001  
 LOCUS 603342751P1 NCI\_CGAP\_Mam2 Mus musculus cDNA clone IMAGE:5370612 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BI692283  
 VERSION BI692283.1 GI:15634912  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC http://mgi.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cga@phs-remai.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L1AM11943 row: e column: 13  
 High quality sequence stop: 800.  
 Location/Qualifiers  
 1..843  
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 /mol\_type="mRNA"  
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 /tissue type="tumor, biopsy sample"  
 /dev stage="5 months"  
 /lab host="DH10B"  
 /clone lib="NCI\_CGAP Mam2"  
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**ORIGIN**  
 Query Match 66.7%; Score 425.4; DB 12; Length 843;  
 Best Local Similarity 84.5%; Pred. No. 6.1e-114;

Matches: 513; Conservative 0; Mismatches 66; Indels 28; Gaps 2;

QY 28 GCTGCTGAGCCATGCTGAGGCGAAATACACACCTTTCACAGCCTGACGAGAGCTTGA 87  
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Db 178 GCTGCTGAGCCATGCTGAGGCGGAGATCAACACCTTTCGAGCCCTGACGAGAGCTTCA 237  
QY 88 ATGCTGCTGAGGATTTACAGAGAGCCCAACCTCTTCTGATGACAAAGCGGCGCACT 147  
Db 238 ACCTGCTCTAGGAATACAAAAAGCCCAACCTCTTCTGATGACAAAGCGGCGCACT 297  
QY 148 TCCTGAGATCTCTTCGATGCGACATGATGAGCAAGGAGGAGGAGGAGGAGGAGGAGG 207  
Db 298 TCTGAGGATCTCTTCGATGCGACATGATGAGCAAGGAGGAGGAGGAGGAGGAGGAGG 357  
QY 208 TTCAGCTGAGCTGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 267  
Db 358 TTGAGC--CAGCTCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 415  
QY 268 GCCAGTACTTGGCCATGACACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 327  
Db 416 GCCAGTACTTGGCCATGACACCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 475  
QY 328 ATGTTGTTTCTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 387  
Db 476 ATGTTGTTTCTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 535  
QY 388 ATGAGAGAGAGATGTTGTTGTTGCTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGG 447  
Db 536 ATGCGAGAGAGAGTGGTTGTTGTTGCTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGG 595  
QY 448 AAATCTACTATGCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 507  
Db 596 GAGCTGCTACTATGCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 655  
QY 508 GAGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 567  
Db 656 GAGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 689  
QY 568 CCCAAAATGTTCCCTTGACCATGCGTGGCTTAACCCCGAGGAGGAGGAGGAGGAGGAGG 627  
Db 690 CCTTACATGTTCCCTTGACCATGCGTGGCTTAACCCCGAGGAGGAGGAGGAGGAGGAGG 749  
QY 628 GTAAGCA 634  
Db 750 GTAAGCA 756

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LOCUS RCL-NN0233-221100-011-h12 NN0233 Homo sapiens cDNA, mRNA sequence.  
DEFINITION BF956865  
VERSION BF956865.1 GI:12374140  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 461)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20203663  
PUBMED 10737800

CONTACT: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RCL&t2=RCL-NN0233-  
221100-011-h12&t3=2000-11-22&t4=1)  
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/notes="Organ: nervous normal; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

# ORIGIN

Query Match 66.5%; Score 424.2; DB 10; Length 461;  
Best Local Similarity 97.8%; Pred. No. 1e-113;  
Matches 451; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

QY 113 GCCAAAGCTCTCTACTGTAGCAAGCGGGGCCACTTCTCTGAG-GATCTCTCCGATGGCA 171  
Db 1 GCGCAAAACA CTTCTACTGTAGCAAGCGGGGCCACTTCTCTGAGAGATCTCTCCGATGGCA 60  
QY 172 CAGTGGATGGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 231  
Db 61 CAGTGGATGGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120  
QY 232 CGTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 291  
Db 121 CGTGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180  
QY 292 ACGGGCTTTTATACGGCTCACAGACACCAATGAGGAATGTTGTTCTCGGAAAGGCTGG 351  
Db 181 ACGGGCTTTTATACGGCTCACAGACACCAATGAGGAATGTTGTTCTCGGAAAGGCTGG 240  
QY 352 AGGAGAACCTTACCAACCTATATATCAAGAGCATGCGAGAGTATGCGGAGGAGGAGGAGG 411  
Db 241 AGGAGAACCTTACCAACCTATATATCAAGAGCATGCGAGAGTATGCGGAGGAGGAGGAGG 300  
QY 412 GCCTCAAGAGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 471  
Db 301 GCCTCAAGAGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360  
QY 472 TCTTGTCTCTCCCTCCGAGGCTCTCTCTGATTAAGAGAGATCTGCT-GGTGTGACCA 530  
Db 361 TCTTGTCTCTCCCTCCGAGGCTCTCTCTGATTAAGAGAGATCTGCTGCTGTGTGACCA 420  
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BC027001 2206 bp mRNA linear HTC 19-NOV-2003  
Mus musculus fibroblast growth factor 1, mRNA (cDNA clone  
IMAGE:5370612), containing frame-shift errors.

ACCESSION BC027001  
VERSION BC027001.1 GI:20073273  
KEYWORDS HTC.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 2206)  
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Dege,J.G.,  
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,  
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,  
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heich,F.,  
Diachenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,  
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,  
Schetz,T.E., Brownstein,M.J., Udén,T.B., Toshiyuki,S.,

Db	406	GCACGTA	CTTGGCCAT	GGACACCGAAGGG	CTTTATACGGCT	CGCAGACACCA	CAATGAG	465				
Qy	328	ATGCTGTG <th>TTGCTCGAAAGCGCT</th> <th>GGAGAGAACCA</th> <th>TTACACACCT</th> <th>TATATATCA</th> <th>CAAGAAGC</th> <td>387</td>	TTGCTCGAAAGCGCT	GGAGAGAACCA	TTACACACCT	TATATATCA	CAAGAAGC	387				
Db	466	ATGCTGTG <th>TTGCTCGAAAGCGCT</th> <th>GGAGAGAACCA</th> <th>TTATACCA</th> <th>TTACACCT</th> <th>CAAGAAGC</th> <td>525</td>	TTGCTCGAAAGCGCT	GGAGAGAACCA	TTATACCA	TTACACCT	CAAGAAGC	525				
Qy	388	ATGCAGAGA <th>AGAAATGGT</th> <th>TTGTTGGCCCTCAAGA</th> <th>GAATGGAGCTGC</th> <th>AAACCGGCTCTA</th> <td>447</td>	AGAAATGGT	TTGTTGGCCCTCAAGA	GAATGGAGCTGC	AAACCGGCTCTA	447					
Db	526	ATCGGAGAGA <th>AGAACTGGT</th> <th>TTGTTGGGCTCAAGA</th> <th>GAACGGAGCTGTAG</th> <th>CCCGCTCTC</th> <td>585</td>	AGAACTGGT	TTGTTGGGCTCAAGA	GAACGGAGCTGTAG	CCCGCTCTC	585					
Qy	448	AAACTCACT <th>ATGGCCAGAAAGCA</th> <th>ATCTGT</th> <th>TTCTTCCCGCTGC</th> <th>CAGCTCTCTCTGA</th> <th>TTAA</th> <td>507</td>	ATGGCCAGAAAGCA	ATCTGT	TTCTTCCCGCTGC	CAGCTCTCTCTGA	TTAA	507				
Db	586	GGACTCACT <th>ATATGGCCAGAAAGCA</th> <th>ATCTGT</th> <th>TTCTTCCCGCTGC</th> <th>CAGCTCTCTCTGA</th> <th>TTAA</th> <td>645</td>	ATATGGCCAGAAAGCA	ATCTGT	TTCTTCCCGCTGC	CAGCTCTCTCTGA	TTAA	645				
Qy	508	GAGATCTGT <th>TTGCTGTGTC</th> <th>CACTCCAGAGAA</th> <th>GTGTTGCA</th> <th>GGGCTCTCACT</th> <th>CGTGTGAC</th> <td>567</td>	TTGCTGTGTC	CACTCCAGAGAA	GTGTTGCA	GGGCTCTCACT	CGTGTGAC	567				
Db	646	GGAGTCTGT <th>CTCT</th> <td data-cs="4" data-kind="parent">-----GAGTGTCTCTATTTTGGTTGA</td> <td data-kind="ghost"></td> <td data-kind="ghost"></td> <td data-kind="ghost"></td> <td>679</td>	CTCT	-----GAGTGTCTCTATTTTGGTTGA				679				
Qy	568	CCCAAAAT <th>GTTCCTCTGAC</th> <th>ATGCTGGCTGGTGA</th> <th>ACCCCAAGCC</th> <th>CAAGAGCTGTA</th> <th>TTT</th> <td>627</td>	GTTCCTCTGAC	ATGCTGGCTGGTGA	ACCCCAAGCC	CAAGAGCTGTA	TTT	627				
Db	680	CCCTAC <th>CAATGTTCCCTTGAC</th> <th>CAATGGCTGGCTGA</th> <th>ACCTCAGGCC</th> <th>CAAGAGCTGTA</th> <th>TTT</th> <td>739</td>	CAATGTTCCCTTGAC	CAATGGCTGGCTGA	ACCTCAGGCC	CAAGAGCTGTA	TTT	739				
Qy	628	GTAAGCA	634									
Db	740	GTAAGCA	746									
RESULT 14												
LOCUS	A1119291											
DEFINITION	ue95c07.y1 Sugano mouse embryo mewa Mus musculus cDNA clone	663 bp	mRNA	linear	EST 02-SEP-1998							
IMAGE:	1498860 5' similar to gb:M13361 HEPARIN-BINDING GROWTH FACTOR											
PRECUSOR	1 (HUMAN), mRNA sequence.											
ACCESSION	A1119291											
VERSION	A1119291.1	GI:3519615										

SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 663)

AUTHORS  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Gaisel, C., Kambam, S., Karsch, W., Kim, J., Kim, M., Kim, Y., Kim,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

**TITLE**  
The WashU-HHMI Mouse EST Project  
**JOURNAL**  
Unpublished (1996)  
**COMMENT**  
Contact: Marria M/Mouse EST Project  
WashU-HHMI Mouse EST Project  
Washington University School of Medicine#  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: [mouseest@watson.wustl.edu](mailto:mouseest@watson.wustl.edu)  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
MG1-936464  
Seq primer: custom primer used  
High quality sequence stored

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        /clone_lib="Sugano mouse embryo newa"
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        Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
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        double-stranded cDNA was ligated to a DraIII adaptor
        [GTGGGCGCTACTGG], digested and cloned into distinct DraIII
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        CACCATGTG). XhoI should be used to isolate the cDNA
        insert. Size: 327 bp."

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insect: size selection was performed to exclude fragments



<1.5kb. Library constructed by Dr. Sumio Sugano  
(University of Tokyo Institute of Medical Science).  
Custom primers for sequencing: 5' end primer  
CTTCTGCTCTAAAGCTGGG and 3' end primer  
CGACCTGACCTCGAGCACA."

ORIGIN

Query Match 64.0%; Score 408.2; DB 9; Length 663;  
Best Local Similarity 89.2%; Pred. No. 6.4e-109;  
Matches 440; Conservative 0; Mismatches 53; Indels 0; Gaps 0;  
QY 28 GCTGCTGAGCAGTGGTGAAGGGGAATACCACTTCTCAGCCTCGAGAGTTT 87  
Db 165 GCTGCGAGCCATGGCTGAAGGGGAGATCACAACTTTCAGCCCTGACCGAGGTTC 224  
QY 88 ATCTGCTCCAGGAATTAACAGAGCCCAAACTCTCTACTGTAGCAAGGGGGCCACT 147  
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QY 208 TTCAAGCTGCACTCAGTGGCGAAAGCGTGGGGAGGTGTATATAAGAGTACCGAGCTG 267  
Db 345 TTCAAGCTGCACTCAGTGGCGAAAGTGGGGAGGTGTATATAAGAGTACCGAGCTG 404  
QY 268 GCGAGTACTTGGCCATGCAAGCGAGCGGGCTTTTATACGGCTTCACAGACCAAAATGAGG 327  
Db 405 GCGAGTACTTGGCCATGCAAGCGAGCGGGCTTTTATACGGCTTCACAGACCAAAATGAGG 464  
QY 328 AATGTTTGTCTCGAAAGCGTGGAGAGCAACATTTATACGGCTTCACAGACCAAAATGAGG 387  
Db 465 AATGTTTGTCTCGAAAGCGTGGAGAGCAACATTTATACGGCTTCACAGACCAAAATGAGG 524  
QY 388 ATGCAAGAGAGATGTTTGTGGCTTCAGAGAGATGGAGCTGCAAGCGCGTCTCTA 447  
Db 525 ATGCGAGAGAGATGTTTGTGGCTTCAGAGAGATGGAGCTGCAAGCGCGTCTCTA 584  
QY 448 AATCTACTATGCGCAAGAGCAATCTGTTCTCCCGCTTCAGAGAGATGGAGCTGCAAGCGCGTCTCTA 507  
Db 585 GATCTACTATGCGCAAGAGCAATCTGTTCTCCCGCTTCAGAGAGATGGAGCTGCAAGCGCGTCTCTA 644  
QY 508 GAGATCTGTTCTG 520  
Db 645 GAGATCTGTTCTG 657

RESULT 15

B1331990  
LOCUS 602984393F1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:5137246 5',  
DEFINITION mRNA sequence.  
ACCESSION B1331990  
VERSION B1331990.1 GI:15016647  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1. (bases 1 to 855)  
NIH-MGC http://mgs.cni.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs@mail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL1337 row: i column: 23  
High quality sequence stop: 752.

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/clone\_lib="NCI CGAP L19"  
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;  
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Technologies. Note: This is a NCI\_CGAP Library."

ORIGIN

Query Match 63.3%; Score 404; DB 12; Length 855;  
Best Local Similarity 89.7%; Pred. No. 1.3e-107;  
Matches 434; Conservative 0; Mismatches 50; Indels 0; Gaps 0;  
QY 28 GCTGCTGAGCAGTGGTGAAGGGGAATACCACTTCTCAGCCTCGAGAGTTT 87  
Db 184 GCTGCGAGCCATGGCTGAAGGGGAGATCACAACTTTCAGCCCTGACCGAGGTTC 243  
QY 88 ATCTGCTCCAGGAATTAACAGAGCCCAAACTCTCTACTGTAGCAAGGGGGCCACT 147  
Db 244 ACTTGCTCTAGGAACTACAAAAGGCCAACTGCTCTACTGCAAGGGGGCCACT 303  
QY 148 TCCTGAGGATCTTCGGATGGCAAGTGGATGGCAAGGGGACGACGACCA 207  
Db 304 TCTTGAGGATCTTCGGATGGCAAGTGGATGGCAAGGGGACGACGACCA 363  
QY 208 TTCAAGCTGCACTCAGTGGCGAAAGCGTGGGGAGGTGTATATAAGAGTACCGAGCTG 267  
Db 364 TTCAAGCTGCACTCAGTGGCGAAAGTGGGGAGGTGTATATAAGAGTACCGAGCTG 423  
QY 268 GCGAGTACTTGGCCATGCAAGCGAGCGGGCTTTTATACGGCTTCACAGACCAAAATGAGG 327  
Db 424 GCGAGTACTTGGCCATGCAAGCGAGCGGGCTTTTATACGGCTTCACAGACCAAAATGAGG 483  
QY 328 AATGTTTGTCTCGAAAGCGTGGAGAGCAACATTTATACGGCTTCACAGACCAAAATGAGG 387  
Db 484 AATGTTTGTCTCGAAAGCGTGGAGAGCAACATTTATACGGCTTCACAGACCAAAATGAGG 543  
QY 388 ATGCAAGAGAGATGTTTGTGGCTTCAGAGAGATGGAGCTGCAAGCGCGTCTCTA 447  
Db 544 ATGCGAGAGAGATGTTTGTGGCTTCAGAGAGATGGAGCTGCAAGCGCGTCTCTA 603  
QY 448 AATCTACTATGCGCAAGAGCAATCTGTTCTCCCGCTTCAGAGAGATGGAGCTGCAAGCGCGTCTCTA 507  
Db 604 GATCTACTATGCGCAAGAGCAATCTGTTCTCCCGCTTCAGAGAGATGGAGCTGCAAGCGCGTCTCTA 663  
QY 508 GAGA 511  
Db 664 GGGA 667

Search completed: August 24, 2004, 20:50:28  
Job time : 2851 secs



## ALIGNMENTS



Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	1	GAATTCGGGAACGGGCTCACAGCAGCAGCAGCTGCTGAGCCATGTGCTGAAAGGGGAAATCACCA	60
Db	1	GAATTCGGGAACGGGCTCACAGCAGCAGCAGCTGCTGAGCCATGTGCTGAAAGGGGAAATCACCA	60
QY	61	CTTTTCACAGCCCTGACCGAGAAGTTTAATCTGCTCTCAGGCAATTACAGAAGCCCAAC	120
Db	61	CTTTTCACAGCCCTGACCGAGAAGTTTAACTCTGCTCTCAGGCAATTACAGAAGCCCAAC	120
QY	121	TCGCTCTACTAGTACAGGGGGGCGACTTCTCTGAGATCTCTCGGATGCGACAGTGGATG	180
Db	121	TCGCTCTACTAGTACAGGGGGGCGACTTCTCTGAGATCTCTCGGATGCGACAGTGGATG	180
QY	181	GGACAAGGGGACAGAGGCGACACAGACATTCAGCTGCGACGCTCATGCGGAAAGGCTGGGG	240
Db	181	GGACAAGGGGACAGAGGCGACACAGACATTCAGCTGCGACGCTCATGCGGAAAGGCTGGGG	240
QY	241	AGGTGTATATAAAGGTACCGAGACTGCGCAGTACTTGGCCATGCGACACGACGGCGTTT	300
Db	241	AGGTGTATATAAAGGTACCGAGACTGCGCAGTACTTGGCCATGCGACACGACGGCGTTT	300
QY	301	TATACGGCTCACAGACACAAATGAGGAATGTTTGTCTCGAAAGGCTGGAGGAGAACC	360
Db	301	TATACGGCTCACAGACACAAATGAGGAATGTTTGTCTCGAAAGGCTGGAGGAGAACC	360
QY	361	ATTACAAACACTATATATCCAAAGCATGACAGAGAAATGTTGTTCTGGAAGGCTGCGAGGACA	420
Db	361	ATTACAAACACTATATCCAAAGCATGCGAGAGAAATGTTGTTCTGGAAGGCTGCGAGGACA	420
QY	421	AGAAATGGAGCTGCGAAACGGGCTCTTAAACTCTATATGCGCAGAAACGAATCTGTTTC	480
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QY	481	TCCCCCTGCCAGTCTCTCTTGATTAAAGAGATCTGTTCTGTTGTGACCACTCCAGAA	540
Db	481	TCCCCCTGCCAGTCTCTCTTGATTAAAGAGATCTGTTCTGTTGTGACCACTCCAGAA	540
QY	541	GTTTTCAGGGGCTGCTCACTGGTTGACCCCAAAAATGTTCCCTGACCATGTGCTGCGCT	600
Db	541	GTTTTCAGGGGCTGCTCACTGGTTGACCCCAAAAATGTTCCCTGACCATGTGCTGCGCT	600
QY	601	AAACCCCAAGCCACAGAGCCTGGAATTTGTAAAGCACTT	638
Db	601	AAACCCCAAGCCACAGAGCCTGGAATTTGTAAAGCACTT	638

## RESULT 4

LOCUS	108090	638 bp	DNA	linear	PAT 02-DEC-1994
DEFINITION	Sequence 4 from Patent EP 0298723.				

ACCESSION I08090  
VERSION I08090.1 GI:589198

**KEYWORDS**  
SOURCE  
Unknown

SOURCE	ORGANISM
Unknown.	Unknown.
Unknown.	Unknown.

Unclassified.  
REFERENCE 1 (bases 1 to 638)

AUTHORS	Fiddes, J.C., Abraham, J.A. and Protter, A.
TITLE	Recombinant fibroblast growth factors

**JOURNAL** Patent: EP 0298723-A1 4 11-JAN-1989;  
**FEATURES** Location/Qualifiers

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Query Match 68.0%; Score 434; DB 6; Length 638;  
Best Local Similarity 100.0%; Pred. No. 4.8e-223;

Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GGCCACAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAATCACCACTTCAGCCC 72

Db  
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73 TGACCGAGAGTTTAATCTGCTCCAGGGAAATTACAAGAGCCCCAACTCCTCTACTGTA 132

db  
125 TGACCGAGAGTTTAACTCTGCTCCAGGGAAATTACAAGAGCCCAACTCTCTACTACTA 184

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QY	133	GCAACGGGGGCGCATTCTTCGTAGGATCTTCCGGATGCGACAGTGGATGGACAAGGGACA	192
Db	185	GCAACGGGGGCGCATTTCTCGAGATCTTCCTCGGATGCGACAGTGGATGGACAAGGGACA	244
QY	193	GGAGCGCACACGCACATTTAGCTGCGACTGTCGGAAGCGTGGGGGAGGTGTATATAA	252
Db	245	GGAGCGCACACGCACATTCAGCTGCGACTGTCGGAAGCGTGGGGGAGGTGTATATAA	304
QY	253	AGAGTACCAGCATGTGGCGCACTAGTCTTGCCCATGSCACACGCGGCTTTTTATACGGCTCAC	312
Db	305	AGAGTACCAGGACTTGGCGCACTAGTCTTGCCCATGSCACACGCGGCTTTTTATACGGCTCAC	364
QY	313	AGACACCAANTGAGGAATGTTTGTCTCGAAAGCGCTGGAGGAGAACCATTACAAACCT	372
Db	365	AGACACCAAAATGAGGAATGTTTGTCTCGAAAGCGCTGGAGGAGAACCATTACAAACCT	424
QY	373	ATATATCCAAGAACATGACAGAGAATTTGGTTTGTGGCTCTAAGAAGAAATGGGAGCT	432
Db	425	ATATATCCAAGAGCATGCACAGAGAATTTGGTTTGTGGCTCTAAGAAGAAATGGGAGCT	484
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Db	485	GCAACGGGGTCTT	498

RESULT 5

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I09138
LOCUS           I09138               638 bp      DNA
DEFINITION     Sequence 3 from Patent WO 8900198.
ACCESSION      I09138
VERSION        I09138.1   GI:588154
KEYWORDS       .
SOURCE         Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 638)
AUTHORS       Fiddes,J.C., Abraham,J.A. and Protter,A.
JOURNAL       Patent: WO 8900198-A 3 12-JAN-1989;
FEATURES             Location/Qualifiers
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Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Dbb 125 TGACCGAGAAGTTTAACTGTGCTCCAGGGAATTACAAGAGCCCAACTCCTCTACTGTA 184

133 GCAACGGGGGCCACTTCTGAGGATCCTTCGGATGGCACAGTGGATGGACAAAGGACA 192

dbb 185 GCAACGGGGGCCACTTCTCGAGGATCCTCCGGATGGCACAGTGGATGGGACAGGGACA 244

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Db 245 GGAGCGACCAAGCATTTCAGCTGCAGCTCAGTGGGAAAGCGTGCGGGAGGTATATAA 304

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b6  
305 AGAGTACCGAGA CTGCTGC ACTA CTTTCGGCA TCCACA CA  
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b7C  
317 GGTATCATGA AATTGAA GTTGCTG ATGCTGTA TTATCCC TCAC  
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[illegible]

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365 AGACACCAATGAGGAATGTTTGTTCTCGGAAGCGCTGGAGGAGAACCATTTACACACCT 424

373 ATATATCCAAAGAAGCATGCAGAGAAGAATTGGTTTGGCCTCAAGAGAATTGGGAGCT 432

425 ATATATCAAGAAGCATGCAGAGAAGAAATGTTTGTGGCTCAAGAAGAATGGGAGCT 484

433 GCAACGGGTCCT 446

\_\_\_\_\_

Db 485 GCMAACGGGTCT 498

RESULT 6

BC032697

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

FEATURES

SOURCE

1. 1073

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/clone="MGC:44867 IMAGE:5403677"

/tissue\_type="Liver, adenocarcinoma"

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BC032697 1073 bp mRNA linear PRI 06-OCT-2003

Homo sapiens fibroblast growth factor 1 (acidic), mRNA (cDNA clone

MGC:44867 IMAGE:5403677), complete cds.

BC032697

BC032697.1 GI:21595686

MGC.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1073)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, P.S., Wagner, K.H., Shenmen, C.M., Schuler, G.D.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.L., Wang, J., Hsieh, F.,

Diachenko, L., Marushin, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Schaefer, T.E., Brownstein, M.J., Ustin, T.B., Casavant, T.L.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Hale, S., Garcia, A.M., Gunaratne, P.H., Richards, S.,

Wyllie, K.C., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahy, J., Hellon, E., Kettman, M., Madan, A., Rodriguez, S.,

Sanchez, J., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitt, R.M.,

Butterfield, Y.S., Krzyzinski, M.I., Skalska, U., Smolius, D.E.,

Schur, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 1073)

Strausberg, R.

Direct Submission

Submitted (06-JUN-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: [nisc.mgc@nih.gov](mailto:nisc.mgc@nih.gov)

Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,

McDowell, J., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,

McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 69 Row: d Column: 4

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 15055546.

Location/Qualifiers

1. 1073

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/db\_xref="taxon:9606"

/clone="MGC:44867 IMAGE:5403677"

/tissue\_type="Liver, adenocarcinoma"

/clone\_lib="NIH\_MGC\_90"

gene

CDS

misc\_feature

ORIGIN

Query Match 68.0%; Score 434; DB 9; Length 1073;  
Best Local Similarity 100.0%; Pred. No. 4.6e-223;  
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCGCCACACAGCAGCAGCTGCTGAGCCATGCTGAAGGGGAATACCAACCTTCACAGCCC 72

DB 65 GCGCCACACAGCAGCAGCTGCTGAGCCATGCTGAAGGGGAATACCAACCTTCACAGCCC 124

QY 73 TCGCCGAGAGTTTAACTTCCTCCAGGGAATTAACAAGAGCCCAACTCTCTACTGTA 132

DB 125 TCGCCGAGAGTTTAACTTCCTCCAGGGAATTAACAAGAGCCCAACTCTCTACTGTA 184

QY 133 GCACGGGGGCGCCTTCTGAGGATCTTCGGATGCGACAGTGATGGGAGGAGGACA 192

DB 185 GCACGGGGGCGCCTTCTGAGGATCTTCGGATGCGACAGTGATGGGAGGAGGACA 244

QY 193 GCAGGGAGCCAGCAGCTGCTGAGGATCTTCGGATGCGACAGTGATGGGAGGAGGACA 252

DB 245 GCAGGGAGCCAGCAGCTGCTGAGGATCTTCGGATGCGACAGTGATGGGAGGAGGACA 304

QY 253 AGAGTACCGAGACTGGCCAGTACTTGGCCATGCGACAGTGATGGGAGGAGGACA 312

DB 305 AGAGTACCGAGACTGGCCAGTACTTGGCCATGCGACAGTGATGGGAGGAGGACA 364

QY 313 AGACACCAATGAGGAATTTTGTTCCTGGAAAGGCTGGAGAGGAGGAGGACA 372

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DB 425 ATATATCCAAAGAGCAGTACAGAGGAATTTGTTGCTTCAAGAGGAGGAGGACA 484

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DB 485 GCAACGCGGCTCT 498

RESULT 7

HSRGP1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Human mRNA for human heparin-binding growth factor 1/acidic

fibroblast growth factor.

X51943

X51943.1 GI:32435

fibroblast growth factor; growth factor; heparin-binding growth

factor.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

LOCUS	AR380845	490 bp	DNA	linear	PAT 18-DEC-2003
DEFINITION	Sequence 1390 from patent US 6607879.				
ACCESSION	AR380845				
VERSION	AR380845.1	GI:40088479			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 490)				
AUTHORS	Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.				
TITLE	Compositions for the detection of blood cell and immunological response gene expression				
JOURNAL	Patent: US 6607879-A 1390 19-AUG-2003;				
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Db	121	CCTGAGGATCTCTTCGGATGACACAGTGGATGGGACAGGAGCCACGACACAT	180		
QY	209	TCAGCTGCAGCTCATGTGCGGAAGCGTGGGGGAGGTGTATATAAAGAGTACCGAGACTGG	268		
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Qy		
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389	TGCAGAGAGAATTTGGTTTGTGGCTTCAAGAGAATGGAGCTGCMAACGGGTCTCT	446
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361	TGCAGAGAGAATTTGGTTTGTGGCTTCAAGAGAATGGAGCTGCMAACGGGTCTCT	418

  

RESULT	9
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DEFINITION	H.sapiens aFGF mRNA for acidic fibroblast growth factor.
ACCESSION	X65778
VERSION	X65778.1 GI:396163
KEYWORDS	fibroblast growth factor; fibroblast growth factor acidic.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Yu, Y.L., Kha.H., Golden,J.A., Migchielsen,A.A., Goetzl,E.J. and Turk,C.W.
TITLE	An acidic fibroblast growth factor protein generated by alternate splicing acts like an antagonist
JOURNAL	J. Exp. Med. 175 (4), 1073-1080 (1992)
MEDLINE	92202857
PUBMED	1372643
FEATURES	Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.2e-214;  
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Db 361 TCAGAGAGATGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAACGGGGTCT 418

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S67291  
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DEFINITION Homo sapiens acidic fibroblast growth factor (aFGF) mRNA, partial cds.  
ACCESSION S67291  
VERSION S67291.1 GI:456823  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Zhao X.M., Yeoh T.K., Hiebert M., Frist W.H. and Miller G.G.  
TITLE The expression of acidic fibroblast growth factor (heparin-binding growth factor-1) and cytokine genes in human cardiac allografts and T cells  
JOURNAL Transplantation 56 (5), 1177-1182 (1993)  
MEDLINE 94069734  
PUBMED 7504343  
REMARK GenBank staff at the National Library of Medicine created this entry (NCBI gi396164070) from the original journal article. This sequence comes from Fig. 2A.  
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TVDTGRSDQHIQLOLSAESVGEVYIKSTGYLMDTDLGLYGSOTPNRECLFLE  
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ORIGIN  
Query Match 63.9%; Score 408; DB 9; Length 464;  
Best Local Similarity 100.0%; Pred. No. 5.7e-209;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 39 ATGCTGAAGGGGAATCAACCTTCACAGCCCTGACCGAAGTTAAATCTGCTCCA 98  
Db 1 ATGCTGAAGGGGAATCAACCTTCACAGCCCTGACCGAAGTTAAATCTGCTCCA 60  
QY 99 GGGAAATTACAAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCACTTCTGAGGATC 158  
Db 61 GGGAAATTACAAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCACTTCTGAGGATC 120  
QY 159 CTTCGGATGGCAGTGGATGGGACAGGACAGGACAGGACAGGACAGGACAGGACAG 218  
Db 121 CTTCGGATGGCAGTGGATGGGACAGGACAGGACAGGACAGGACAGGACAGGACAG 180  
QY 219 CTGATGCGAAGAGCGTGGGGAGGTGTATTAAGAGTACCGAGACTGGCCAGTACTG 278  
Db 181 CTGATGCGAAGAGCGTGGGGAGGTGTATTAAGAGTACCGAGACTGGCCAGTACTG 240  
QY 279 GCCATGACACCAAGCGGCTTTTATACGGCTCAGACACCAATTAAGAGTACCGAGACTGGCCAGTACTG 338  
Db 241 GCCATGACACCAAGCGGCTTTTATACGGCTCAGACACCAATTAAGAGTACCGAGACTGGCCAGTACTG 300  
QY 339 CTGAAAGCGTGGAGAGAACCAATTAACCACTATATATCAAGAGCATGCGAGAG 398  
Db 301 CTGAAAGCGTGGAGAGAACCAATTAACCACTATATATCAAGAGCATGCGAGAG 360  
QY 399 AATTGTTTGTGGCTCAAGAGAAATGGGAGCTGCAACGGGGTCT 446  
Db 361 AATTGTTTGTGGCTCAAGAGAAATGGGAGCTGCAACGGGGTCT 408

RESULT 11  
AR428605  
LOCUS AR428605 468 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 3 from patent US 6642026.  
ACCESSION AR428605  
VERSION AR428605.1 GI:40188276  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 468)  
AUTHORS Stegmann, T.J., Kordyum, V.A., Slavchenko, I.Yu., Chernykh, S.I. and Vozianov, O.P.  
TITLE Method of producing biologically active human acidic fibroblast growth factor and its use in promoting angiogenesis  
JOURNAL Patent: US 6642026-A 3 04-NOV-2003;  
FEATURES  
source  
Location/Qualifiers  
1..468  
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ORIGIN  
Query Match 63.9%; Score 408; DB 6; Length 468;  
Best Local Similarity 100.0%; Pred. No. 5.7e-209;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 39 ATGCTGAAGGGGAATCAACCTTCACAGCCCTGACCGAAGTTAAATCTGCTCCA 98  
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QY 99 GGGAAATTACAAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCACTTCTGAGGATC 158  
Db 61 GGGAAATTACAAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCACTTCTGAGGATC 120  
QY 159 CTTCGGATGGCAGTGGATGGGACAGGACAGGACAGGACAGGACAGGACAGGACAG 218  
Db 121 CTTCGGATGGCAGTGGATGGGACAGGACAGGACAGGACAGGACAGGACAGGACAG 180  
QY 219 CTGATGCGAAGAGCGTGGGGAGGTGTATTAAGAGTACCGAGACTGGCCAGTACTG 278

Db 181 CTAGTGGGAAAGCGTGGGGAGGTGTATATAAGAGTACCGAGACTGGCAGTACTTG 240  
QY 279 GCCATGACACCGACCGGGCTTTTATACGGCTCAGACAGCAACCAATGAGAAATGTTTGTTC 338  
Db 241 GCCATGACACCGACCGGGCTTTTATACGGCTCAGACAGCAACCAATGAGAAATGTTTGTTC 300  
QY 339 CTGGAAGGCTGGAGGAGACCAATTAACAACCTATATATCAAGAGCATGACAGAGAG 398  
Db 301 CTGGAAGGCTGGAGGAGACCAATTAACAACCTATATATCAAGAGCATGACAGAGAG 360  
QY 399 AATTGGTTTGTGGCTCAGAGAGATGGGAGCTGCAAGCGGTCT 446  
Db 361 AATTGGTTTGTGGCTCAGAGAGATGGGAGCTGCAAGCGGTCT 408

RESULT 12  
AX481449  
LOCUS AX481449 468 bp DNA linear PAT 16-AUG-2002  
DEFINITION Sequence 63 from Patent WO02055693.  
ACCESSION AX481449  
VERSION AX481449.1 GI:22316363  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Kreutzer, R., Limmer, S., Rost, S. and Hadwiger, P.  
TITLE Method for inhibiting the expression of a target gene  
JOURNAL Patent: WO 02055693-A 63 18-JUL-2002;  
Ribopharma AG (DE)  
FEATURES  
source Location/Qualifiers  
1..468  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
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ORIGIN  
Query Match 63.9%; Score 408; DB 6; Length 468;  
Best Local Similarity 100.0%; Pred. No. 5.7e-209;  
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QY 99 GGAATTAACAAGAGCCCAAACTCTCTACTGTAGCAAGCGGGCCCACTTCTCAGAGTC 158  
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QY 219 CTCAGTGGGAAAGCGTGGGGAGGTGTATATAAGAGTACCGAGACTGGCCAGTACTTG 278  
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Db 241 GCCATGACACCGACCGGGCTTTTATACGGCTCAGACAGCAACCAATGAGAAATGTTTGTTC 300  
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Db 301 CTGGAAGGCTGGAGGAGACCAATTAACAACCTATATATCAAGAGCATGACAGAGAG 360  
QY 399 AATTGGTTTGTGGCTCAGAGAGATGGGAGCTGCAAGCGGTCT 446  
Db 361 AATTGGTTTGTGGCTCAGAGAGATGGGAGCTGCAAGCGGTCT 408

RESULT 13  
A49428  
LOCUS A49428 8501 bp DNA circular PAT 07-MAR-1997  
DEFINITION Sequence 1 from Patent WO9608572.  
ACCESSION A49428  
VERSION A49428.1 GI:2302907  
KEYWORDS

SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 8501)  
AUTHORS Cameron, B. and Crouzet, J.  
TITLE METHOD FOR THE PRODUCTION OF RECOMBINANT PROTEINS, PLASMIDS AND MODIFIED CELLS  
JOURNAL Patent: WO 9608572-A 1 21-MAR-1996;  
RHONE-POULENC RORER SA (FR)  
COMMENT Other publication AU 3475495 960329  
Other publication FR 2724665 960322.  
FEATURES  
source Location/Qualifiers  
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ORIGIN  
Query Match 63.9%; Score 408; DB 6; Length 8501;  
Best Local Similarity 100.0%; Pred. No. 4.5e-209;  
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QY 99 GGAATTAACAAGAGCCCAAACTCTCTACTGTAGCAAGCGGGCCCACTTCTCAGAGTC 158  
Db 168 GGAATTAACAAGAGCCCAAACTCTCTACTGTAGCAAGCGGGCCCACTTCTCAGAGTC 227  
QY 159 CTCCTGGATGCGACAGTGGATGGGAGGACAGGAGGACGACGACATTCAGCTGCAG 218  
Db 228 CTCCTGGATGCGACAGTGGATGGGAGGACAGGAGGACGACGACATTCAGCTGCAG 287  
QY 219 CTCAGTGGGAAAGCGTGGGGAGGTGTATATAAGAGTACCGAGACTGGCCAGTACTTG 278  
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QY 279 GCCATGACACCGACCGGGCTTTTATACGGCTCAGACAGCAACCAATGAGAAATGTTTGTTC 338  
Db 348 GCCATGACACCGACCGGGCTTTTATACGGCTCAGACAGCAACCAATGAGAAATGTTTGTTC 407  
QY 339 CTGGAAGGCTGGAGGAGACCAATTAACAACCTATATATCAAGAGCATGACAGAGAG 398  
Db 408 CTGGAAGGCTGGAGGAGACCAATTAACAACCTATATATCAAGAGCATGACAGAGAG 467  
QY 399 AATTGGTTTGTGGCTCAGAGAGATGGGAGCTGCAAGCGGTCT 446  
Db 468 AATTGGTTTGTGGCTCAGAGAGATGGGAGCTGCAAGCGGTCT 515

RESULT 14  
I08499  
LOCUS I08499 481 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 13 from Patent WO 8701728.  
ACCESSION I08499  
VERSION I08499.1 GI:588791  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 481)  
AUTHORS Fiddes, J.C. and Abraham, J.A.  
TITLE RECOMBINANT FIBROBLAST GROWTH FACTORS  
JOURNAL Patent: WO 8701728-A 13 26-MAR-1987;  
FEATURES  
source Location/Qualifiers  
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Query Match 56.3%; Score 359; DB 6; Length 481;  
Best Local Similarity 99.8%; Pred. No. 1.9e-182;  
Matches 409; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 37 CCATGGCTGAAGGGGAAATCAACCACTTCACAGCCCTGACCGAGAGTTTAAATCTGCTCC 96  
Db 1 CCATGGCTGAAGGGGAAATCAACCACTTCACAGCCCTGACCGAGAGTTTAAATCTGCTCC 60



QY 97 CAGGGAATTACAAAGAGCCCAACTCTCTACTGTAGCAAGGGGGCCACTTCTCGAGA 156  
Db 61 CAGGGAATTACAAAGAGCCCAACTCTCTACTGTAGCAAGGGGGCCACTTCTCGAGA 120  
QY 157 TCCTTCGGATGGCAGATGGATGGGACAGAGGACAGGAGGACACCAATTCAGCTGC 216  
Db 121 TCCTTCGGATGGCAGATGGATGGGACAGAGGACAGGAGGACACCAATTCAGCTGC 180  
QY 217 AGCTCAGTGGGAAAGCGTGGGGAGGTGTATATAAGAGTACCGAGACTGGCCAGTACT 276  
Db 181 AGCTCAGTGGGAAAGCGTGGGGAGGTGTATATAAGAGTACCGAGACTGGCCAGTACT 240  
QY 277 TGGCCATGGACACCGAGCGGGCTTTATACGGCTTCACACCAATTCAGGAAATGTTGT 336  
Db 241 TGGCTATGGACACCGAGCGGGCTTTATACGGCTTCACACCAATTCAGGAAATGTTGT 300  
QY 337 TCTGGAAGGCTGGAGAGACCAATACACACCTATATATCCAGAGCATGCGAGAGA 396  
Db 301 TCTGGAAGGCTGGAGAGACCAATACACACCTATATATCCAGAGCATGCGAGAGA 360  
QY 397 AGAATGTTGTTGGCTTCAGAGAAATGGAGCTGCAAAACCGGCTCT 446  
Db 361 AGAATGTTGTTGGCTTCAGAGAAATGGAGCTGCAAAACCGGCTCT 410

RESULT 15  
109297  
LOCUS 109297 481 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 10 from Patent WO 8902471.  
ACCESSION 109297  
VERSION 109297.1 GI:588003  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 481)  
AUTHORS Talmadge,K.D. and Hilliker,S.  
TITLE RECOMBINANT DNA CONSTRUCTS CONTAINING AN r3 PROMOTER  
JOURNAL Patent: WO 8902471-A 10 23-MAR-1989;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 56.3%; Score 359; DB 6; Length 481;  
Best Local Similarity 99.8%; Pred. No. 1.9e-182;  
Matches 409; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 37 CCATGGCTCAGAGGGAATCACCACCTTCAGAGCCCTGACGAGAGTTTAATTCGCTC 96  
Db 1 CCATGGCTCAGAGGGAATCACCACCTTCAGAGCCCTGACGAGAGTTTAATTCGCTC 60  
QY 97 CAGGGAATTACAAAGAGCCCAACTCTCTACTGTAGCAAGGGGGCCACTTCTCGAGA 156  
Db 61 CAGGGAATTACAAAGAGCCCAACTCTCTACTGTAGCAAGGGGGCCACTTCTCGAGA 120  
QY 157 TCCTTCGGATGGCAGATGGATGGGACAGAGGACAGGAGGACACCAATTCAGCTGC 216  
Db 121 TCCTTCGGATGGCAGATGGATGGGACAGAGGACAGGAGGACACCAATTCAGCTGC 180  
QY 217 AGCTCAGTGGGAAAGCGTGGGGAGGTGTATATAAGAGTACCGAGACTGGCCAGTACT 276  
Db 181 AGCTCAGTGGGAAAGCGTGGGGAGGTGTATATAAGAGTACCGAGACTGGCCAGTACT 240  
QY 277 TGGCCATGGACACCGAGCGGGCTTTATACGGCTTCACACCAATTCAGGAAATGTTGT 336  
Db 241 TGGCTATGGACACCGAGCGGGCTTTATACGGCTTCACACCAATTCAGGAAATGTTGT 300  
QY 337 TCTGGAAGGCTGGAGAGACCAATACACACCTATATATCCAGAGCATGCGAGAGA 396  
Db 301 TCTGGAAGGCTGGAGAGACCAATACACACCTATATATCCAGAGCATGCGAGAGA 360  
QY 397 AGAATGTTGTTGGCTTCAGAGAAATGGAGCTGCAAAACCGGCTCT 446  
Db 361 AGAATGTTGTTGGCTTCAGAGAAATGGAGCTGCAAAACCGGCTCT 410

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Title: US-10-022-554A-3  
Perfect score: 638  
Sequence: 1 gaattcggaagcgcacacccccctgaattgtaagcaactt 638

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

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Minimum DB seq length: 0

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5: Geneseqn2001bs.\*  
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8: Geneseqn2003bs.\*  
9: Geneseqn2003cs.\*  
10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	638	100.0	638	8	ACF04029 Thrombin
2	485	76.0	638	1	Aan70788 Complete
3	485	76.0	638	2	AAT37503 Human bet
4	485	76.0	638	2	AAV34350 Human end
5	485	76.0	638	2	AAV34350 Human end
6	485	76.0	638	8	ACF04028 Thrombin
7	444	69.6	639	2	AAT45985 Human end
8	434	68.0	638	1	AAN93088 Human fib
9	434	68.0	2357	9	ACC42968 Human fib
10	434	68.0	4087	7	ABX63225 Human GDN
11	408	63.9	468	6	ABV78179 Human DNA
12	408	63.9	468	6	ABZ35755 Human pol
13	408	63.9	468	6	ABX09998 Human DNA
14	408	63.9	468	6	AAK98918 Human aci
15	408	63.9	468	6	ABL91720 Human pol
16	408	63.9	8501	2	AAT12907 Novel exp
17	405	63.5	462	2	AAT45983 Human end
18	359	56.3	481	1	AAN71029 Sequence
19	359	56.3	481	1	AAN90994 Partially
20	345	54.1	408	3	AAC66107 Human PGF
21	345	54.1	408	9	ADD68672 Human DNA
22	345	54.1	434	9	ADD68674 Human DNA
23	345	54.1	516	2	AAK81395 Polynucle
24	345	54.1	525	2	AAK81379 Polynucle
25	345	54.1	525	3	AAC66108 Chimeric
26	345	54.1	525	3	AAC66109 Chimeric



27 345 54.1 537 3 AAC66128 Mutant FG  
28 345 54.1 537 3 AAC66129 Mutant FG  
29 345 54.1 546 9 ADD68675 DNA ampli  
30 345 54.1 546 9 ADD68676  
31 345 54.1 600 2 AAX81392  
32 345 54.1 600 2 AAX81391  
33 345 54.1 602 9 ADD68692  
34 345 54.1 630 2 AAX81396  
35 345 54.1 647 9 ADD68691  
36 345 54.1 663 2 AAX81378  
37 345 54.1 707 9 ADD68686  
38 345 54.1 707 9 ADD68690  
39 345 54.1 762 2 AAX81393  
40 345 54.1 843 2 AAX81394  
41 309 48.4 405 2 AAT45984  
42 258 40.4 540 2 AAX81397  
43 255 40.0 543 2 AAX81380  
44 254 39.8 540 3 AAC66126  
45 253 39.7 540 3 AAC66130

#### ALIGNMENTS

RESULT 1  
ACF04029  
ID ACF04029 standard; DNA; 638 BP.  
XX  
AC ACF04029;  
XX  
DT 15-OCT-2003 (first entry)  
XX  
DE Thrombin resistant FGF-1 mutant coding sequence.  
XX  
KW Thrombin resistant FGF-1; FGF-1; fibroblast growth factor-1;  
KW myocardial ischaemia; peripheral vascular disease; cerebral ischaemia;  
KW epithelial injury; epidermal wound injury; nerve injury; mutant;  
KW bone damage; vasoprotective; cardiatic; cerebroprotective; vulnerary;  
KW neuroprotective; osteopathic; gene; ds.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT CDS 42..506  
FT /tag= a  
FT /product= "FGF-1 mutant"  
FT /partial  
FT /note= "no start codon"  
XX  
PN M02003052378-A2.  
XX  
PD 26-JUN-2003.  
XX  
PF 11-DEC-2002; 2002WO-US039686.  
XX  
PR 17-DEC-2001; 2001US-00022554.  
XX  
PA (REPA-) REPAIR INC.  
PA (MAIN-) MAINE MEDICAL CENT RES INST.  
XX  
PI Maciag T, Ettenson DS, Burgess WH, Drohan WN;  
XX  
DR WPI; 2003-559052/52.  
XX P-PSDB; ABR63869.  
XX  
DE New thrombin degradation resistant fibroblast growth factor-1 (FGF-1)  
XX polypeptide, useful for treating a disease or disorder, e.g. cerebral  
XX ischaemia or bone damage, or for enhancing the effectiveness of an FGF-1  
XX response in a mammal.  
XX  
PS Claim 1; Fig 10; 83pp; English.  
XX  
CC The present invention provides the protein and coding sequences of human  
CC fibroblast growth factor-1 (FGF-1) and a mutant that is resistant to  
CC thrombin degradation. The thrombin degradation resistant FGF-1 protein  
CC can be used for treating a disease or disorder (e.g. myocardial  
CC ischaemia, peripheral vascular disease, cerebral ischaemia, epithelial  
CC injury, epidermal wound injury, nerve injury, or bone damage), for

CC enhancing the effectiveness of an FGF-1 response, or for stimulating an  
CC FGF-1 response in a mammal. The present sequence is the mutant FGF-1  
CC coding sequence  
XX  
SQ Sequence 638 BP; 175 A; 164 C; 166 G; 133 T; 0 U; 0 Other;  
Query Match 100.0%; Score 638; DB 8; Length 638;  
Best Local Similarity 100.0%; Pred. No. 1.8e-304;  
Matches 638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAATTCGGGAACCGCCCAAGCAGCAGCTGCTGAGCCATGCTGAGAGGGGGAATCCCA 60  
Db 1 GAATTCGGGAACCGCCCAAGCAGCAGCTGCTGAGCCATGCTGAGAGGGGGAATCCCA 60  
QY 61 CCTTCACAGCCCTGACCCAGCAGCTTATCTGCTCCAGGGAATTTACAAGACCCCAAC 120  
Db 61 CCTTCACAGCCCTGACCCAGCAGCTTATCTGCTCCAGGGAATTTACAAGACCCCAAC 120  
QY 121 TCTCTACTGTAGCAACGGGGGCCACTTCTGAGGATCTTCCGATGCGCAGTGGATG 180  
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QY 181 GGACAGGGGACAGGAGGACGACGACATTCAGTCTGAGCTCAGTCTGAGGAGGAGG 240  
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QY 241 AGGTGTATATAAGAGTACCGAGACTGCGCCAGTCTGCGCCAGTCTGCGCCAGTCT 300  
Db 241 AGGTGTATATAAGAGTACCGAGACTGCGCCAGTCTGCGCCAGTCTGCGCCAGTCT 300  
QY 301 TATACGCTCAGACACACCAATGAGGATGTTTCTTGGAAAGGCTGAGGAGAAC 360  
Db 301 TATACGCTCAGACACACCAATGAGGATGTTTCTTGGAAAGGCTGAGGAGAAC 360  
QY 361 ATTACACACCTATATATCCAAAGACATGCGAGAGAGTGTGTTGGCTTCAAGA 420  
Db 361 ATTACACACCTATATATCCAAAGACATGCGAGAGAGTGTGTTGGCTTCAAGA 420  
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QY 481 TCCCTCTGCGAGCTCTCTCTGATTAAGAGATCTGCTGCTGCTGCTGCTGCTGCT 540  
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QY 601 AACCCCAACCCACACAGAGCTGGAATTTGAGCAACTT 638  
Db 601 AACCCCAACCCACACAGAGCTGGAATTTGAGCAACTT 638

RESULT 2  
AAN70788  
ID AAN70788 standard; cDNA; 638 BP.  
XX  
AC AAN70788;  
XX  
DT 25-MAR-2003 (revised)  
DT 13-MAY-1991 (first entry)  
XX  
DE Complete cDNA sequence of human endothelial cell growth factor (ECGF).  
XX Endothelial cell regeneration, blood vessel regeneration; ss.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 39..506  
FT /tag= a  
FT mat\_peptide 42..83  
FT /tag= b  
FT /product= "Beta ECGF"  
FT 84..101  
FT mat\_peptide  
FT /tag= c  
FT /product= "Acidic FGF"

Db	541	CTTTCGAGGGGCTCTACCTGGTGTGACCCAAAATGTTCCCTTGACCATTTGGCTGGCT	600
Qy	601	AAACCCCGACCCACAGAGCCTGTAATTGTAAAGCAACTT	638
Db	601	AAACCCCGACCCACAGAGCCTGTAATTGTAAAGCAACTT	638
RESULT 3			
AAT37503			
ID	AAT37503	standard; DNA; 638 BP.	
AC	AAT37503;		
XX			
DT	25-MAR-2003	(revised)	
DT	29-DEC-1996	(first entry)	
XX			
DE	Human beta-endothelial cell growth factor.		
XX			
KW	Endothelial cell growth factor; ECGF; blood vessel; regeneration;		
KW	heparin-Sepharose affinity chromatography; probe; oligonucleotide; FGF;		
KW	fibroblast growth factor; ss.		
OS	Homo sapiens.		
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PH	Key	Location/Qualifiers	
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FT		/*tag= b	
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FT		/*tag= d	
FT		/label= alpha-ECGF	
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PN	US5552528-A.		
PD			
PD	03-SEP-1996.		
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PF	03-NOV-1994;	94US-00334884.	
XX			
PR	03-MAR-1986;	86US-00835594.	
PR	18-DEC-1987;	87US-00134499.	
PR	29-APR-1991;	91US-00693079.	
PR	27-NOV-1991;	91US-00799859.	
XX			
PA	(RHON ) RHONE POULENC RORER PHARM INC.		
PI	Maciag T, Burgess W;		
XX			
DR	WPI; 1996-412132/41.		
DR	P-PSDB; AAW04805, AAW04806, AAW04807.		
XX			
PT	Isolated, purified, biologically active bovine beta endothelial cell		
PT	growth factor - useful to regenerate or treat damaged blood vessels.		
XX			
PS	Disclosure; Fig 8; 28pp; English.		
XX			
CC	Bovine beta-endothelial cell growth factor (beta-ECGF; AAW03999) having a		
CC	mol.wt. of 20 kD can be purified at least 16300 fold from bovine brain		
CC	using heparin-Sepharose affinity chromatography. ECGF is useful for,		
CC	among other purposes, diagnostic applications and has potential in the		
CC	treatment of damaged blood vessels or other endothelial cell-lined		
CC	structures. Human ECGF (AAT37503) or fragments may be obtained using		
CC	oligonucleotides (AAT37504 and AAT37508 to AAT37509) whose design is		
CC	based on the sequence of bovine alpha- and beta-ECGF. (Updated on 25-MAR-		
CC	2003 to correct PF field.)		
XX			
SSQ	Sequence 638 BP; 172 A; 145 C; 168 G; 133 T; 0 U; 0 Other;		
Query Match			
Best Local Similarity	76.0%; Score 485; DB 2; Length 638;		
Matches 635; Conservative	0; Mismatches 3; Indels 0; Gaps 0;		
1	GAATTCGGAGACGCCACAGCAGCTGTGTCAGCCATCTGGCTGAGGGGAATACCA	60	

DB 1 GAATTGGGAAACGCGCCCAAGCAGCAGCTGCTGAGCCATGCTGAAAGGGGAATCACCA 60  
 QY 61 CTTTACAGCCCTGACCCAGAGGTTTAAATCTGCTCCAGGGAATACAGAGCCCAAC 120  
 DB 61 CTTTACAGCCCTGACCCAGAGGTTTAAATCTGCTCCAGGGAATACAGAGCCCAAC 120  
 QY 121 TCCTTCTACTGTAGCAACCGGGGCCACTTCTGAGGATCTTCCGGATGCGACAGTGGATG 180  
 DB 121 TCCTTCTACTGTAGCAACCGGGGCCACTTCTGAGGATCTTCCGGATGCGACAGTGGATG 180  
 QY 181 GGACAAAGGACAGAGCGGACGACGATCTCAGCTGCGAGCTGCGGAAAGGCTGGGGG 240  
 DB 181 GGACAAAGGACAGAGCGGACGACGATCTCAGCTGCGAGCTGCGGAAAGGCTGGGGG 240  
 QY 241 AGGTGTATATAAGAGTACCGAGCTGCGGATGCTTGGCTGACGACGAGCGGCTTT 300  
 DB 241 AGGTGTATATAAGAGTACCGAGCTGCGGATGCTTGGCTGACGACGAGCGGCTTT 300  
 QY 301 TATAGCGCTCAGACAGCAACAAATGAGGATGTTTCTCTGGAAGGCTGGAGAGAAC 360  
 DB 301 TATAGCGCTCAGACAGCAACAAATGAGGATGTTTCTCTGGAAGGCTGGAGAGAAC 360  
 QY 361 ATTACACACCTATATATCCAAAGAGCATGCAAGAGAAATGGTTTGGCTCAAGA 420  
 DB 361 ATTACACACCTATATATCCAAAGAGCATGCAAGAGAAATGGTTTGGCTCAAGA 420  
 QY 421 AGAATGGGAGCTGCAAGCGGCTTAAACTCACTATGCGGAAAGGCTGGGGG 480  
 DB 421 AGAATGGGAGCTGCAAGCGGCTTAAACTCACTATGCGGAAAGGCTGGGGG 480  
 QY 481 TCCCTTCTGAGGATCTTCTGATTAAGAGATCTGTTCTGGTGTGACCACTCCAGAGAA 540  
 DB 481 TCCCTTCTGAGGATCTTCTGATTAAGAGATCTGTTCTGGTGTGACCACTCCAGAGAA 540  
 QY 541 GTTTCGAGGGGCTGCAAGCGGCTTAAACTCACTATGCGGAAAGGCTGGGGG 600  
 DB 541 GTTTCGAGGGGCTGCAAGCGGCTTAAACTCACTATGCGGAAAGGCTGGGGG 600  
 QY 601 AACCCCGAGCCACAGAGGCTGAAATTTGTAAGCACTT 638  
 DB 601 AACCCCGAGCCACAGAGGCTGAAATTTGTAAGCACTT 638

RESULT 4  
 ANV34350  
 ID ANV34350 standard; cDNA; 638 BP.  
 AC ANV34350;  
 XX  
 XX 02-MAR-1999 (first entry)  
 XX Human endothelial cell growth factor gene.  
 XX Human, endothelial cell growth factor; ECGF; brain stem; probe;  
 XX hybridisation; bovine; wound healing; prosthetic device; ss.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 XX CDS 39..506  
 FT /\*tag= a  
 FT /product= "precursor ECGF"  
 FT /note= "endothelial cell growth factor"  
 XX  
 PN US5827826-A.  
 XX  
 XX 27-OCT-1998.  
 XX  
 XX 04-NOV-1996; 96US-00743261.  
 XX  
 XX 03-MAR-1986; 86US-00835594.  
 XX 18-DEC-1987; 87US-00134499.  
 XX 29-APR-1991; 91US-00693079.  
 XX 27-NOV-1991; 91US-00799859.  
 XX 03-NOV-1994; 94US-0034884.  
 XX 07-JUN-1995; 95US-00472964.  
 XX  
 XX (RHON ) RHONE-POULENC RORER PHARM INC.

PI Jaye M, Burgess W, Maciag T, Drohan WN;  
 XX WPI; 1998-594032/50.  
 XX P-PSDB; AAW75415.  
 XX  
 PT Compositions for promoting wound healing - containing endothelial cell  
 XX growth factor polypeptides.  
 XX  
 PS Example; Fig 8; 23pp; English.  
 XX  
 CC This sequence represents the complete cDNA sequence encoding both human  
 CC alpha- and beta-endothelial cell growth factors (ECGF; AAW75413-W75414).  
 CC The sequence was isolated from a human brain stem cell cDNA library using  
 CC a probe designed based on fragments of the bovine ECGF (see AAW75416-  
 CC W75418). The ECGF protein can be used in compositions for promoting wound  
 CC healing. ECGF is also used to grow cells on a prosthetic device  
 XX  
 SQ Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;  
 XX  
 Query Match 76.0%; Score 485; DB 2; Length 638;  
 Best Local Similarity 99.5%; Pred. No. 5.9e-229;  
 Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GAATTGGGAAACGCGCCCAAGCAGCAGCTGCTGAGCCATGCTGAAAGGGGAATCACCA 60  
 DB 1 GAATTGGGAAACGCGCCCAAGCAGCAGCTGCTGAGCCATGCTGAAAGGGGAATCACCA 60  
 QY 61 CTTTACAGCCCTGACCCAGAGGTTTAAATCTGCTCCAGGGAATACAGAGCCCAAC 120  
 DB 61 CTTTACAGCCCTGACCCAGAGGTTTAAATCTGCTCCAGGGAATACAGAGCCCAAC 120  
 QY 121 TCCTTCTACTGTAGCAACCGGGGCCACTTCTGAGGATCTTCCGGATGCGACAGTGGATG 180  
 DB 121 TCCTTCTACTGTAGCAACCGGGGCCACTTCTGAGGATCTTCCGGATGCGACAGTGGATG 180  
 QY 181 GGACAAAGGACAGAGCGGACGACGATCTCAGCTGCGAGCTGCGGAAAGGCTGGGGG 240  
 DB 181 GGACAAAGGACAGAGCGGACGACGATCTCAGCTGCGAGCTGCGGAAAGGCTGGGGG 240  
 QY 241 AGGTGTATATAAGAGTACCGAGCTGCGGATGCTTGGCTGACGACGAGCGGCTTT 300  
 DB 241 AGGTGTATATAAGAGTACCGAGCTGCGGATGCTTGGCTGACGACGAGCGGCTTT 300  
 QY 301 TATAGCGCTCAGACAGCAACAAATGAGGATGTTTCTCTGGAAGGCTGGAGAGAAC 360  
 DB 301 TATAGCGCTCAGACAGCAACAAATGAGGATGTTTCTCTGGAAGGCTGGAGAGAAC 360  
 QY 361 ATTACACACCTATATATCCAAAGAGCATGCAAGAGAAATGGTTTGGCTCAAGA 420  
 DB 361 ATTACACACCTATATATCCAAAGAGCATGCAAGAGAAATGGTTTGGCTCAAGA 420  
 QY 421 AGAATGGGAGCTGCAAGCGGCTTAAACTCACTATGCGGAAAGGCTGGGGG 480  
 DB 421 AGAATGGGAGCTGCAAGCGGCTTAAACTCACTATGCGGAAAGGCTGGGGG 480  
 QY 481 TCCCTTCTGAGGATCTTCTGATTAAGAGATCTGTTCTGGTGTGACCACTCCAGAGAA 540  
 DB 481 TCCCTTCTGAGGATCTTCTGATTAAGAGATCTGTTCTGGTGTGACCACTCCAGAGAA 540  
 QY 541 GTTTCGAGGGGCTGCAAGCGGCTTAAACTCACTATGCGGAAAGGCTGGGGG 600  
 DB 541 GTTTCGAGGGGCTGCAAGCGGCTTAAACTCACTATGCGGAAAGGCTGGGGG 600  
 QY 601 AACCCCGAGCCACAGAGGCTGAAATTTGTAAGCACTT 638  
 DB 601 AACCCCGAGCCACAGAGGCTGAAATTTGTAAGCACTT 638

RESULT 5  
 AAX01723  
 ID AAX01723 standard; cDNA; 638 BP.  
 AC AAX01723;  
 XX  
 XX 20-APR-1999 (first entry)  
 XX Human endothelial cell growth factor (ECGF) cDNA sequence.  
 XX Endothelial cell growth factor; ECGF; cleavable; recombinant; repair;  
 XX

KW Regenerate; blood vessel; endothelial cell; human; ss.  
 XX Homo sapiens.  
 OS Key Location/Qualifiers  
 XX CDS 39..506  
 FT /\*tag= a  
 FT /product= "ECGF"  
 FT misc\_feature 42  
 FT /\*tag= b  
 FT /note= "beta-ECGF begins at this position"  
 FT misc\_feature 84  
 FT /\*tag= c  
 FT /note= "acidic EGF begins at this position"  
 FT misc\_feature 102  
 FT /\*tag= d  
 FT /note= "alpha-ECGF begins at this position"  
 XX  
 PV US5849538-A.  
 XX  
 XX 15-DEC-1998.  
 XX  
 XX 11-APR-1997; 97US-00840088.  
 XX  
 XX 03-MAR-1986; 86US-00835594.  
 XX 18-DEC-1987; 87US-00134499.  
 XX 29-APR-1991; 91US-00693079.  
 XX 27-NOV-1991; 91US-00799859.  
 XX 03-NOV-1994; 94US-00334884.  
 XX 07-JUN-1995; 95US-00472964.  
 XX 04-NOV-1996; 96US-00743261.  
 XX  
 XX (RHON ) RHONE-POULENC RORER PHARM INC.  
 XX  
 XX Jaye M, Burgess W, Maciag T, Drohan WN;  
 XX WPI: 1999-069734/06.  
 XX P-PSDB; AAW92291.  
 XX  
 XX DNA encoding a cleavable signal peptide and an endothelial cell growth factor - useful for producing recombinant endothelial cell growth factor proteins.  
 XX  
 XX Disclosure; Fig 8; 23pp; English.  
 XX  
 XX The invention relates to DNA encoding human endothelial cell growth factors (ECGF) and plasmids comprising the DNA sequences. The DNA encodes a cleavable signal peptide and an ECGF, where removal of the signal peptide yields a mature form of the ECGF, where the ECGF is alpha-ECGF or beta-ECGF. The DNA is used to produce recombinant ECGF proteins, which can be used in treatments to repair or regenerate blood vessels or other structures lined with endothelial cells. The present sequence represents a human ECGF cDNA sequence (determined from lambda ECGF clones 1 and 29)  
 XX  
 XX Sequence 638 BP; 172 A; 165 C; 168 G; 133 T; 0 U; 0 Other;  
 SQ  
 Query Match 76.0%; Score 485; DB 2; Length 638;  
 Best Local Similarity 99.5%; Pred. No. 5.9e-229;  
 Matches 635; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GAATTCGGGAACGGCCGACAGCAGCAGCTCTGAGCCATCGCTGAAGGGGAATCACCA 60  
 Db |||||||  
 QY 1 GAATTCGGGAACGGCCGACAGCAGCAGCTCTGAGCCATCGCTGAAGGGGAATCACCA 60  
 Db |||||||  
 QY 61 CTTTCCACAGCCCTGACCCAGAGAGTTTAACTCTGCTCCAGGGAATTACAGAGCCCAAC 120  
 Db |||||||  
 QY 61 CTTTCCACAGCCCTGACCCAGAGAGTTTAACTCTGCTCCAGGGAATTACAGAGCCCAAC 120  
 Db |||||||  
 QY 121 TCCTCTACTGTAGCAACGGGGGCCACTTCTCTGAGGATCTTTCGGATGGCAGATGGATG 180  
 Db |||||||  
 QY 121 TCCTCTACTGTAGCAACGGGGGCCACTTCTCTGAGGATCTTTCGGATGGCAGATGGATG 180  
 Db |||||||  
 QY 181 GGACAGGAGCAGAGGACGACGACATTCAGCTGACCTCAGTGGGAAAGCGTGGGG 240  
 Db |||||||  
 QY 181 GGACAGGAGCAGAGGACGACGACATTCAGCTGACCTCAGTGGGAAAGCGTGGGG 240  
 Db |||||||  
 QY 241 AGGTGTATATAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGCGGCTTT 300  
 Db |||||||  
 QY 241 AGGTGTATATAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGACACCGCGGCTTT 300  
 Db |||||||

QY 301 TATACGGCTCAGACACCAATGAGGAATGTTTGTTCCTGGAAAGCTGGAGGAGACC 360  
 Db |||||||  
 QY 301 TATACGGCTCAGACACCAATGAGGAATGTTTGTTCCTGGAAAGCTGGAGGAGACC 360  
 Db |||||||  
 QY 361 ATTACAAACCTATATATCCAGAGAGCATCCAGAGAGAAATGTTTGTGGCTCAAGA 420  
 Db |||||||  
 QY 361 ATTACAAACCTATATATCCAGAGAGCATCCAGAGAGAAATGTTTGTGGCTCAAGA 420  
 Db |||||||  
 QY 421 AGAATGGAGCTGCAAAAGCGGCTCTAAACTCATTATGGCCAGAAAGCAATCTGTTTC 480  
 Db |||||||  
 QY 421 AGAATGGAGCTGCAAAAGCGGCTCTCGGACTCACTATGGCCAGAAAGCAATCTGTTTC 480  
 Db |||||||  
 QY 481 TCCCTCTCCAGTCTCTCTGATTAAGAGATCTGTCTGTGTGACCACTCCAGAGAA 540  
 Db |||||||  
 QY 481 TCCCTCTCCAGTCTCTCTGATTAAGAGATCTGTCTGTGTGACCACTCCAGAGAA 540  
 Db |||||||  
 QY 541 GTTTCGAGGGGCTCTCACTGTTGACCCCAAAAATGTTCCCTTGACCATTTGCTGCGCT 600  
 Db |||||||  
 QY 541 GTTTCGAGGGGCTCTCACTGTTGACCCCAAAAATGTTCCCTTGACCATTTGCTGCGCT 600  
 Db |||||||  
 QY 601 AACCCCGAGCCACAGAGCGCTGAAATTTGTAGCAACTT 638  
 Db |||||||  
 QY 601 AACCCCGAGCCACAGAGCGCTGAAATTTGTAGCAACTT 638  
 Db |||||||  
 RESULT 6  
 ID ACF04028 standard; DNA; 638 BP.  
 XX AC ACF04028;  
 XX  
 DT 15-OCT-2003 (first entry)  
 XX  
 XX Thrombin resistant FGF-1 mutant production wildtype coding sequence.  
 XX  
 XX Thrombin resistant FGF-1; FGF-1; fibroblast growth factor-1;  
 XX myocardial ischaemia; peripheral vascular disease; cerebral ischaemia;  
 XX epithelial injury; epidermal wound injury; nerve injury; bone damage;  
 XX vasotrophic; cardiant; cerebroprotective; vulnerary; neuroprotective;  
 XX osteopathic; gene; ds.  
 XX  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 XX CDS 42..506  
 FT /\*tag= a  
 FT /product= "FGF-1"  
 FT /partial  
 FT /note= "no start codon"  
 XX  
 XX WO2003052378-A2.  
 XX  
 XX 26-JUN-2003.  
 XX  
 XX 11-DEC-2002; 2002WO-US039686.  
 XX  
 XX 17-DEC-2001; 2001US-00022554.  
 XX  
 XX (REPA-) REPAIR INC.  
 XX (MAIN-) MAINE MEDICAL CENT RES INST.  
 XX  
 XX Maciag T, Ebbenson DS, Burgess WH, Drohan WN;  
 XX  
 XX WPI; 2003-559052/52.  
 XX P-PSDB; ABR63868.  
 XX  
 XX New thrombin degradation resistant fibroblast growth factor-1 (FGF-1)  
 XX polypeptide, useful for treating a disease or disorder, e.g. cerebral  
 XX ischaemia or bone damage, or for enhancing the effectiveness of an FGF-1  
 XX response in a mammal.  
 XX  
 XX Claim 2; Fig 8; 83pp; English.  
 XX  
 XX The present invention provides the protein and coding sequences of human  
 XX fibroblast growth factor-1 (FGF-1) and a mutant that is resistant to  
 XX thrombin degradation. The thrombin degradation resistant FGF-1 protein  
 XX can be used for treating a disease or disorder (e.g. myocardial  
 XX ischaemia, peripheral vascular disease, cerebral ischaemia, epithelial

\_\_\_\_\_

10

RESULT 8  
 AAN93088  
 ID AAN93088 standard; DNA; 638 BP.  
 XX  
 AC AAN93088;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 25-JUN-1990 (first entry)  
 XX  
 DE Acidic fibroblast growth factor.  
 XX  
 KW Acidic fibroblast growth factor; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT mat\_peptide 91..555  
 FT /\*tag= a  
 FT /label= human acidic fibroblast growth factor  
 XX  
 EP298723-A.  
 XX  
 PD 11-JAN-1989.  
 XX  
 PF 06-JUL-1988; 88EP-00306158.  
 XX  
 PR 07-JUL-1987; 87US-00070797.  
 XX  
 PA (BIOU ) BIOTECH RES INST.  
 XX  
 PI Fides JC, Abraham JA, Protter A;  
 DR WPI; 1989-009785/02.  
 DR N-PSDB; AAN93087.  
 XX  
 PT Recombinant DNA encoding new fibroblast growth factor analogues - useful  
 PT e.g. for accelerating wound healing and to control neovascularisation.  
 XX  
 PS Disclosure; Fig 2; 44pp; English.  
 XX  
 CC The sequence encodes human acidic fibroblast growth factor (aFGF). See  
 CC also AAN93087 and AAN93089. (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 638 BP; 170 A; 156 C; 168 G; 144 T; 0 U; 0 Other;  
 XX  
 Query Match 68.0%; Score 434; DB 1; Length 638;  
 Best Local Similarity 100.0%; Pred. No. 8.7e-204;  
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 GCGCCACAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAATCACCACCTTCACAGCCC 72  
 DB 65 GCGCCACAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAATCACCACCTTCACAGCCC 124  
 QY 73 TGACCCGAGAGCTTTAATCTGCTCCAGGGAATTACAAGAGCCCAAACTCTCTACTGTA 132  
 DB 125 TGACCCGAGAGCTTTAATCTGCTCCAGGGAATTACAAGAGCCCAAACTCTCTACTGTA 184  
 QY 133 GCAACGGGGCCACTTCTGAGGATCTTCCGGATGGCAAGTGGATGGCAAGGACA 192  
 DB 185 GCAACGGGGCCACTTCTGAGGATCTTCCGGATGGCAAGTGGATGGCAAGGACA 244  
 QY 193 GGAGGACCGAGCATTCAGCTGCACTCAGTCCGGAAGCGTGGGGAGGTGTATATA 252  
 DB 245 GGAGGACCGAGCATTCAGCTGCACTCAGTCCGGAAGCGTGGGGAGGTGTATATA 304  
 QY 253 AGAGTACCGAGCTGCGCAGTCTGCGCATGGCAAGCGGGCTTTTATACGGCTAC 312  
 DB 305 AGAGTACCGAGCTGCGCAGTCTGCGCATGGCAAGCGGGCTTTTATACGGCTAC 364  
 QY 313 AGACACCAATAGGAATGTTTGTCTGGAAGGCTGGAGGAACTTACACACT 372  
 DB 365 AGACACCAATAGGAATGTTTGTCTGGAAGGCTGGAGGAACTTACACACT 424  
 QY 373 ATATATCCAGAGCATTCAGAGAGATTTGTTTGTGGCTTCAAGAGATTTGGAGCT 432  
 DB 425 ATATATCCAGAGCATTCAGAGAGATTTGTTTGTGGCTTCAAGAGATTTGGAGCT 484  
 QY 433 GCAACGGGTCTCT 446  
 |||||||

DB 485 GCAACGGGTCTCT 498  
 RESULT 9  
 ACC42968  
 ID ACC42968 standard; DNA; 2357 BP.  
 XX  
 AC ACC42968;  
 XX  
 DT 18-DEC-2003 (first entry)  
 DT  
 DE Human Fibroblast Growth Factor 1 coding sequence.  
 XX  
 KW Human; Fibroblast Growth Factor 1; FGF1, acidic FGF; aFGF;  
 KW acidic Fibroblast Growth Factor; protein co-ordinate data; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 142..609  
 FT /\*tag= a  
 FT /product= "FGF1"  
 XX  
 WO2003038054-A2.  
 XX  
 PD 08-MAY-2003.  
 XX  
 PF 31-OCT-2002; 2002WO-US034986.  
 XX  
 PR 31-OCT-2001; 2001US-0335583P.  
 XX  
 PA (UINNY ) UNIV NEW YORK STATE.  
 XX  
 PI Moosa M, Green DL, Linhard RJ;  
 DR WPI; 2003-482144/45.  
 DR P-PSDB; ABR56165.  
 XX  
 PT Composition useful for identifying modulators of fibroblast growth factor  
 PT -mediated signaling for use in treating cancer, has ternary complex of  
 PT FGF-receptor, FGF ligand and heparin agonist or antagonist.  
 XX  
 PS Disclosure; Fig 16B; 288pp; English.  
 XX  
 CC The present invention relates to an isolated composition comprising a  
 CC ternary complex of an Fibroblast Growth Factor (FGF) ligand polypeptide  
 CC (ABR56163, ABR56165), an FGF receptor polypeptide (ABR56164) and a  
 CC heparin agonist or antagonist, where the agonist or antagonist binds to  
 CC the FGF ligand polypeptide and the FGF receptor polypeptide to form the  
 CC ternary complex. The composition is useful for identifying a compound  
 CC that is an inhibitor of FGF receptor activity. FGF1 is also known as  
 CC acidic FGF  
 XX  
 SQ Sequence 2357 BP; 691 A; 521 C; 567 G; 578 T; 0 U; 0 Other;  
 XX  
 Query Match 68.0%; Score 434; DB 9; Length 2357;  
 Best Local Similarity 100.0%; Pred. No. 8.4e-204;  
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 GCGCCACAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAATCACCACCTTCACAGCCC 72  
 DB 116 GCGCCACAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAATCACCACCTTCACAGCCC 175  
 QY 73 TGACCCGAGAGCTTTAATCTGCTCCAGGGAATTACAAGAGCCCAAACTCTCTACTGTA 132  
 DB 176 TGACCCGAGAGCTTTAATCTGCTCCAGGGAATTACAAGAGCCCAAACTCTCTACTGTA 235  
 QY 133 GCAACGGGGCCACTTCTGAGGATCTTCCGGATGGCAAGTGGATGGCAAGGACA 192  
 DB 236 GCAACGGGGCCACTTCTGAGGATCTTCCGGATGGCAAGTGGATGGCAAGGACA 295  
 QY 193 GGAGGACCGAGCATTCAGCTGCACTCAGTCCGGAAGCGTGGGGAGGTGTATATA 252  
 DB 296 GGAGGACCGAGCATTCAGCTGCACTCAGTCCGGAAGCGTGGGGAGGTGTATATA 355  
 QY 253 AGAGTACCGAGCTGCGCAGTCTGCGCATGGCAAGCGGGCTTTTATACGGCTAC 312  
 DB 356 AGAGTACCGAGCTGCGCAGTCTGCGCATGGCAAGCGGGCTTTTATACGGCTAC 415

QY 313 AGACACCAATGAGGAATGTTTCTCTGGAAGGCTGAGGAGAACCAATTACACACCT 372  
DB 416 AGACACCAATGAGGAATGTTTCTCTGGAAGGCTGAGGAGAACCAATTACACACCT 475  
QY 373 ATATATCCAAAGAGATGCGAGAGAAATGGTTTGGGCTTCAAGAGAAATGGAGCT 432  
DB 476 ATATATCCAAAGAGATGCGAGAGAAATGGTTTGGGCTTCAAGAGAAATGGAGCT 535  
QY 433 GCACACGGGGTCT 446  
DB 536 GCACACGGGGTCT 549

RESULT 10  
ID ABX63225 standard; cDNA; 4087 BP.  
XX  
AC ABX63225;  
XX  
DT 25-FEB-2003 (first entry)  
XX  
DE Human cDNA #225 differentially expressed in activated vascular tissue.  
XX  
KW Human; gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiac;  
KW hypotensive; antidiabetic; gynaecological; vasotropic; cerebroprotective;  
KW gene therapy; vascular disease; cancer; coronary; artery disease;  
KW hypertension; diabetes; pre-eclampsia; restenosis;  
KW ischaemia-reperfusion injury; stroke.  
XX  
OS Homo sapiens.  
XX  
PN US2002137081-A1.  
XX  
PD 26-SEP-2002.  
XX  
PF 08-JAN-2002; 2002US-00044090.  
XX  
PR 28-JUL-2000; 2000US-0222469P.  
PR 08-JAN-2001; 2001US-0260483P.  
XX  
PA (BAND/) BANDMAN O.  
XX  
PI Bandman O;  
XX  
DR WPI; 2003-110597/10.  
XX  
PT Combination for diagnosing, staging, treating, or monitoring the  
PT progression of treatment of a vascular disease, e.g. atherosclerosis,  
PT comprises several cDNAs that are differentially expressed in activated  
PT vascular tissue.  
XX  
PS Claim 1; Page; 18pp; English.

CC This invention relates to a combination comprising several cDNAs that are  
CC differentially expressed in activated vascular tissue. The invention also  
CC discloses a high throughput method for detecting differentially expressed  
CC cDNAs in a sample. The cDNAs of the invention may have  
CC antiarteriosclerotic; cytostatic; cardiac; hypotensive; antidiabetic;  
CC gynaecological; vasotropic and cerebroprotective activities and may be  
CC used in gene therapy. The cDNAs of the invention may be used in a high-  
CC throughput methods for detecting differential expression of one or more  
CC cDNAs in a sample, or screening several molecules or compounds to  
CC identify a molecule or compound that specifically binds a cDNA of the  
CC invention. A protein encoded by the cDNA may be used to screen several  
CC molecules or compounds to identify a ligand that specifically binds to  
CC the protein, or to produce or purify an antibody to the protein that can  
CC be used to detect a protein in a sample or purify a natural or  
CC recombinant protein from a sample. The nucleotides may be useful for  
CC diagnosing, staging, treating, or monitoring the progression of treatment  
CC of a vascular disease, e.g. atherosclerosis, cancer, coronary artery  
CC injury, restenosis, or stroke. The cDNAs can also be used for large-scale  
CC genetic or gene expression analysis of several new nucleic acid  
CC molecules. Antibodies to the proteins encoded by the cDNAs are useful for  
CC diagnosing pre-pathologic disorders, and chronic or acute diseases  
CC associated with abnormalities in the expression, amount or distribution  
CC of the protein. The present sequence represents a cDNA of the invention  
CC that is differentially expressed in activated vascular tissue. Note: The  
CC sequence data for this patent did not form part of the specification, but

CC was obtained in electronic format directly from USPTO at  
CC http://seqdata.uspto.gov/sequence.html?DocID=20020137081  
XX  
SQ Sequence 4087 BP; 1164 A; 886 C; 959 G; 1078 T; 0 U; 0 Other;  
Query Match 68.0%; Score 434; DB 7; Length 4087;  
Best Local Similarity 100.0%; Pred. No. 8.3e-204;  
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 13 GCACCAACGAGCAGCTGCTGAGCCATGCTGAGGGGAAATCACCACCTTTCAGAGCC 72  
DB 480 GCACCAACGAGCAGCTGCTGAGCCATGCTGAGGGGAAATCACCACCTTTCAGAGCC 539  
QY 73 TGACCGAGAGTTTAACTGCTCCAGGAAATTCAGAGAGCCCAAACTCTCTACTGTA 132  
DB 540 TGACCGAGAGTTTAACTGCTCCAGGAAATTCAGAGAGCCCAAACTCTCTACTGTA 599  
QY 133 GCACCGGGGCCACTTCTGAGGATCTTCCGATGCGACATGCGATGGGCAAGGGACA 192  
DB 600 GCACCGGGGCCACTTCTGAGGATCTTCCGATGCGACATGCGATGGGCAAGGGACA 659  
QY 193 GAGGAGCAGCAGACATTCAGCTGCGAGCTCAGTCCGAAAGCGTGGGGAGGTGTATATA 252  
DB 660 GAGGAGCAGCAGACATTCAGCTGCGAGCTCAGTCCGAAAGCGTGGGGAGGTGTATATA 719  
QY 253 AGATACCGAGCAGCTGGCCAGTACTTGGCCATGCGACACCGAGGGCTTTATACGGCTCAC 312  
DB 720 AGATACCGAGCAGCTGGCCAGTACTTGGCCATGCGACACCGAGGGCTTTATACGGCTCAC 779  
QY 313 ACACACCAATGAGGAATGTTTCTCTGGAAGGCTGAGGAGAACCAATTACACACCT 372  
DB 780 ACACACCAATGAGGAATGTTTCTCTGGAAGGCTGAGGAGAACCAATTACACACCT 839  
QY 373 ATATATCCAAAGAGATGCGAGAGAAATGGTTTGGGCTTCAAGAGAAATGGAGCT 432  
DB 840 ATATATCCAAAGAGATGCGAGAGAAATGGTTTGGGCTTCAAGAGAAATGGAGCT 899  
QY 433 GCACACGGGGTCT 446  
DB 900 GCACACGGGGTCT 913  
RESULT 11  
ABV78179  
ID ABV78179 standard; DNA; 468 BP.  
XX  
AC ABV78179;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Human DNA SEQ ID NO 63.  
XX  
KW RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic;  
KW virucide; protoroacide; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200255693-A2.  
XX  
PD 18-JUL-2002.  
XX  
PF 09-JAN-2002; 2002WO-EP0000152.  
XX  
PR 09-JAN-2001; 2001DE-01000586.  
PR 26-OCT-2001; 2001DE-01055280.  
PR 29-NOV-2001; 2001DE-01058411.  
PR 07-DEC-2001; 2001DE-01060151.  
XX  
PA (RIBO-) RIBOPHARMA AG.  
XX  
PI Kretzler R, Limmer S, Roat S, Hadwiger P;  
XX  
DR WPI; 2002-590671/63.  
XX  
PT Inhibiting expression of target gene, useful e.g. for inhibiting  
PT oncogenes, by administering double-stranded RNA complementary to the  
PT target and having an overhang.  
XX  
PS Claim 10; Page 147; 203pp; German.

XX CC The invention relates to inhibiting expression of a target gene (I) in a cell by introducing an inhibitory RNA (dsRNA) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (as1) of dsRNA is complementary to (I) and at least one end of dsRNA has an overhang of 1-4 nucleotides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes etc. in humans, also genes in Plasmodium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into dsRNA greatly increases effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of a gene related to the invention

XX SQ Sequence 468 BP; 131 A; 115 C; 126 G; 96 T; 0 U; 0 Other;

Query Match 63.9%; Score 408; DB 6; Length 468;  
Best Local Similarity 100.0%; Pred. No. 6e-191;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATGGCTGAGGGGAATCACCACCTTCAGAGCCCTCAGAGAGTTTAAATCTGCTCCA 98  
DB 1 ATGGCTGAGGGGAATCACCACCTTCAGAGCCCTCAGAGAGTTTAAATCTGCTCCA 60

QY 99 GGGAAATTACAGAGCCCAAACTCTCTCTAGTACCAAGGGGGCCACTTCCTGAGGATC 158  
DB 61 GGGAAATTACAGAGCCCAAACTCTCTCTAGTACCAAGGGGGCCACTTCCTGAGGATC 120

QY 159 CTTCGGATGGCAGTGGATGGGAGGAGTGTATATAAGAGTACCGAGCTGCGGAGT 218  
DB 121 CTTCGGATGGCAGTGGATGGGAGGAGTGTATATAAGAGTACCGAGCTGCGGAGT 180

QY 219 CTCAGTCCGGAAGCGTGGGGAGGTTTATATAAGAGTACCGAGCTGCGGAGT 278  
DB 181 CTCAGTCCGGAAGCGTGGGGAGGTTTATATAAGAGTACCGAGCTGCGGAGT 240

QY 279 GCATATGACACCGAGCGGCTTTTATAGGCTCAGACACCAATAGGAATGTTTCTC 338  
DB 241 GCATATGACACCGAGCGGCTTTTATAGGCTCAGACACCAATAGGAATGTTTCTC 300

QY 339 CTGGAAGGCTGGAGGAGAACCATTTACACCTATATATCCAGAGCATGCGAGAG 398  
DB 301 CTGGAAGGCTGGAGGAGAACCATTTACACCTATATATCCAGAGCATGCGAGAG 360

QY 399 AATTGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAACCGGCTCT 446  
DB 361 AATTGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAACCGGCTCT 408

RESULT 12  
ABZ35755  
ID ABZ35755 standard; DNA; 468 BP.  
AC ABZ35755;  
XX 07-FEB-2003 (first entry)  
DE Human polynucleotide SEQ ID NO 63.  
XX Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;  
KW prozoacide; gene expression; antisense; tumour; infection; Plasmodium;  
KW virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;  
KW Hepatitis C virus; human papilloma virus; gene; ds.  
OS Homo sapiens.  
XX DE10100588-AL.  
XX 18-JUL-2002.  
XX 09-JAN-2001; 2001DE-01000588.  
XX 09-JAN-2001; 2001DE-01000588.  
XX (RIBO-) RIBOPHARMA AG.  
XX Kreutzer R, Limmer S, Rost S, Hadwiger P;  
XX WPI; 2002-683450/74.

XX FT Inhibiting expression of target genes, useful e.g. for treating tumors, by introducing into cells two double-stranded RNAs that are complementary to the target.

XX PS Claim 13; Page 44; 100pp; German.

XX CC The invention relates to inhibiting expression of a target gene in a cell by introducing at least two oligonucleotides (dsRNA and II), both with a double-stranded (ds) structure of at most 49 sequential nucleotide pairs. At least part of one strand (S1, S2) of the ds structures in each of dsRNA and II are complementary to regions in the target gene. The RNA inhibition (RNAi). The method is particularly used to treat tumours or infections, especially by Plasmodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the end, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with interferon. The present sequence is that of a target DNA of the invention

XX SQ Sequence 468 BP; 131 A; 115 C; 126 G; 96 T; 0 U; 0 Other;

Query Match 63.9%; Score 408; DB 6; Length 468;  
Best Local Similarity 100.0%; Pred. No. 6e-191;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATGGCTGAGGGGAATCACCACCTTCAGAGCCCTCAGAGAGTTTAAATCTGCTCCA 98  
DB 1 ATGGCTGAGGGGAATCACCACCTTCAGAGCCCTCAGAGAGTTTAAATCTGCTCCA 60

QY 99 GGGAAATTACAGAGCCCAAACTCTCTCTAGTACCAAGGGGGCCACTTCCTGAGGATC 158  
DB 61 GGGAAATTACAGAGCCCAAACTCTCTCTAGTACCAAGGGGGCCACTTCCTGAGGATC 120

QY 159 CTTCGGATGGCAGTGGATGGGAGGAGTGTATATAAGAGTACCGAGCTGCGGAGT 218  
DB 121 CTTCGGATGGCAGTGGATGGGAGGAGTGTATATAAGAGTACCGAGCTGCGGAGT 180

QY 219 CTCAGTCCGGAAGCGTGGGGAGGTTTATATAAGAGTACCGAGCTGCGGAGT 278  
DB 181 CTCAGTCCGGAAGCGTGGGGAGGTTTATATAAGAGTACCGAGCTGCGGAGT 240

QY 279 GCATATGACACCGAGCGGCTTTTATAGGCTCAGACACCAATAGGAATGTTTCTC 338  
DB 241 GCATATGACACCGAGCGGCTTTTATAGGCTCAGACACCAATAGGAATGTTTCTC 300

QY 339 CTGGAAGGCTGGAGGAGAACCATTTACACCTATATATCCAGAGCATGCGAGAG 398  
DB 301 CTGGAAGGCTGGAGGAGAACCATTTACACCTATATATCCAGAGCATGCGAGAG 360

QY 399 AATTGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAACCGGCTCT 446  
DB 361 AATTGGTTTGTGGCTCAAGAGAAATGGGAGCTGCAACCGGCTCT 408

RESULT 13  
ABX09998  
ID ABX09998 standard; DNA; 468 BP.  
XX AC ABX09998;  
XX 23-JAN-2003 (first entry)  
XX Human DNA fragment SEQ ID 63.  
XX Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;  
KW prion; inhibition; human; ds.  
XX Homo sapiens.  
XX DE10100587-Cl.  
XX 21-NOV-2002.  
XX 09-JAN-2001; 2001DE-01000587.  
XX 09-JAN-2001; 2001DE-01000587.  
XX 09-JAN-2001; 2001DE-01000587.



PH	Key	Location/Qualifiers
FT	CDS	122..589
FT		/tag= a
FT		/product= "Protein of human acidic fibroblast growth factor (155AA)"
XX		
PN		WO200214468-A2.
PD		
PD		21-FEB-2002..
PF		15-AUG-2001; 2001WO-US025477..
PF		15-AUG-2000; 2000US-0225437P.
PR		(PHAG-) PHAGE BIOTECHNOLOGY CORP.
PA		
PI		Kordyum VA, Chernykh SI, Slavchenko IY, Vozianov OF;
XX		WPI; 2002-269184/31.
DR		P-PSDB; AAO19980.
XX		
PT		Bacteriophage-dependent method for producing biologically active proteins or peptides, involves employing an Escherichia coli transformed with a plasmid containing the targeted gene(s) operably linked to a promoter.
PT		
PT		Disclosure; Page 36-37; 44pp; English.
XX		
CC		The invention relates to a method for enhancing the production of a biologically active protein comprising infecting a strain of Escherichia coli, which has been transformed with a plasmid having at least one copy of an expressible gene, such as a human acidic fibroblast growth factor. The expressible gene encodes a biologically active protein operably linked to a phage T7 polymerase promoter, with a bacteriophage capable of mediating delayed lysis. The method is useful for the phage dependent superproduction of biologically active protein and peptides. The method is particularly useful for enhancing the production of heterologous proteins in bacterial host cells. This polynucleotide sequence represents the DNA of a human acidic fibroblast growth factor - FGF Ir HUMECCFB of the invention.
XX		
XX		Sequence 468 BP; 131 A; 115 C; 126 G; 96 T; 0 U; 0 Other;
XX		
XX		Query Match 63.9%; Score 408; DB 6; Length 468;
XX		Best Local Similarity 100.0%; Pred. No. 6e-191;
XX		Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY		39 ATGGCTGAAGGGGAATACCACTTCTACAGCCCTGACCGAGAAGTTTAATCTGCCTCCA 98
Db		
QY		1 ATGGCTGAAGGGGAATACCACTTCTACAGCCCTGACCGAGAAGTTTAATCTGCCTCCA 60
Db		
QY		99 GCGAATTACAGAAGCCCAAACTCTCTACTGTAGCACGGGGGCCACTTCTGAGATC 158
Db		
QY		61 GCGAATTACAGAAGCCCAAACTCTCTACTGTAGCACGGGGGCCACTTCTGAGATC 120
Db		
QY		159 CTTCCGGANTGGCAKAGTGGATGGAGTGGAGGACAGGAGCAGCACCAATTCAGCTGCAG 218
Db		
QY		121 CTTCCGATGGCAGATGGATGGGACAGGAGCAGGAGCAGCACCAATTCAGCTGCAG 180
Db		
QY		219 CTCAGTCGGAAGCGTGGGGAGGTGTATATAAGATGACCGAGCTGGCCAGTACTTG 278
Db		
QY		181 CTCAGTCGGAAGCGTGGGGAGGTGTATATAAGATGACCGAGCTGGCCAGTACTTG 240
Db		
QY		279 GCCATGGACACCGAGCGGCTTTTATACGGCTACACAGACCAAAATGAGGATGTTGTC 338
Db		
QY		241 GCCATGGACACCGAGCGGCTTTTATACGGCTACACAGACCAAAATGAGGATGTTGTC 300
Db		
QY		339 CTGGAAAGGCTGGAGGAGACCAATTAACAACCTTATATCCAAAGACATGCAGAGAAG 398
Db		
QY		301 CTGGAAAGGCTGGAGGAGACCAATTAACAACCTTATATCCAAAGACATGCAGAGAAG 360
Db		
QY		399 AATTGGTTTGTGGCCTCAAGAGAAATGGGAGCTGCAAAGCGGTCT 446
Db		
QY		361 AATTGGTTTGTGGCCTCAGAAAGAAATGGGAGCTGCAAAGCGGTCT 408
Db		
XX		
XX		RESULT 15
XX		ABL91720
XX		ABL91720 standard; DNA; 468 BP.

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Job time : 443 secs

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 20:52:07 ; Search time 86 Seconds
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        4116.961 Million cell updates/sec

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Perfect score: 638
Sequence: 1 gaattcggaacgcgcaca.....cctgaattgtgaacactt 638

Scoring table: OLIGO NJC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES

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No.	Score	Query	Length	ID	Description
1	434	68.0	638	US-09-098-628-3	Sequence 3, Appli
2	418	65.5	490	US-09-023-655-1390	Sequence 1390, Ap
3	408	63.9	468	US-09-929-945-3	Sequence 3, Appli
4	408	63.9	8501	US-08-793-900-1	Sequence 1, Appli
5	186	29.2	454	6 5175147-1	Patent No. 5175147
6	172	27.0	197	6 5514566-3	Patent No. 5514566
7	118	18.5	450	6 5437995-1	Patent No. 5437995
8	77	12.1	454	3 US-09-030-613-14	Sequence 14, Appl
9	77	12.1	454	4 US-09-451-905-14	Sequence 14, Appl
10	26	4.1	630	6 US-09-929-945-1	Sequence 1, Appli
11	24	3.8	270	6 5514566-1	Patent No. 5514566
12	23	3.6	44	1 US-08-023-757-8	Sequence 8, Appli
13	23	3.6	44	1 US-08-177-502-8	Sequence 8, Appli
14	23	3.6	44	1 US-08-054-650A-2	Sequence 2, Appli
15	23	3.6	44	2 US-08-383-621-11	Sequence 11, Appl
16	23	3.6	44	3 US-08-459-906-11	Sequence 11, Appl
17	23	3.6	261	6 5514566-12	Patent No. 5514566
18	23	3.6	45	1 US-08-023-757-1	Sequence 1, Appli
19	23	3.6	45	1 US-08-023-757-3	Sequence 3, Appli
20	23	3.6	45	1 US-07-783-694-1	Sequence 1, Appli
21	23	3.6	465	1 US-07-783-694-2	Sequence 2, Appli
22	23	3.6	465	1 US-08-177-502-1	Sequence 1, Appli
23	23	3.6	465	1 US-08-177-502-3	Sequence 3, Appli
24	23	3.6	471	1 US-08-290-373B-15	Sequence 15, Appl
25	23	3.6	477	1 US-08-290-373B-16	Sequence 16, Appl
26	21	3.3	59	3 US-09-030-613-25	Sequence 25, Appl
27	21	3.3	59	4 US-09-451-905-25	Sequence 25, Appl
28	21	3.3	630	4 US-09-929-945-4	Sequence 4, Appli
29	21	3.3	630	4 US-09-929-945-6	Sequence 6, Appli

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Sequence 26, Appl  
Sequence 26, Appl  
Sequence 159, App  
Sequence 159, App  
Sequence 197, App  
Sequence 208, App  
Sequence 22, Appl  
Sequence 22, Appl  
Sequence 621, App  
Sequence 621, App  
Sequence 202, App  
Sequence 202, App  
Sequence 2657, App  
Sequence 2657, App  
Sequence 16, Appl  
Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-09-098-628-3  
; Sequence 3, Application US/09098628  
; Patent No. 6294359  
; GENERAL INFORMATION:  
; APPLICANT: RIDDES, J.C.  
; APPLICANT: ABRAHAM, J.D.  
; TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH  
; TITLE OF INVENTION: FACTOR ANALOG  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/098,628  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lehnhardt, Susan K  
; REGISTRATION NUMBER: 33,943  
; REFERENCE/DOCKET NUMBER: 21900-20089.10  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO. 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 638 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: Coding Sequence  
; LOCATION: 91...555  
; OTHER INFORMATION:  
US-09-098-628-3

Query Match 68.0%; Score 434; DB 3; Length 638;  
Best Local Similarity 100.0%; Pred. No. 6.3e-217;  
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 13 GCCTCCACGACGAGCTGCTGAGCCATGCTGAGGGGAAATCACCACCTTCACAGCC 72  
DB 65 GCCTCCACGACGAGCTGCTGAGCCATGCTGAGGGGAAATCACCACCTTCACAGCC 124

QY 73 TGACCCGAGAGATTAAATCTGCTCCAGGGAATTAAGAGCCCAAACTCTCTTACTGTA 132  
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QY 193 GAGAGCAGCAGCATTCTGAGCTCAGTGCAGAAAGCTGGGGGAGGTGTATATAA 252  
DB 245 GAGAGCAGCAGCATTCTGAGCTCAGTGCAGAAAGCTGGGGGAGGTGTATATAA 304  
QY 253 AGAGTACCGAGACTGGCCAGTACTTGGCCATGACACAGCGGGCTTTTATAGGCTCAC 312  
DB 305 AGAGTACCGAGACTGGCCAGTACTTGGCCATGACACAGCGGGCTTTTATAGGCTCAC 364  
QY 313 AGACACCAATGAGAAATGTTTCTGCTGGAAGGCTGGAGGAGCAATTAACACACT 372  
DB 365 AGACACCAATGAGAAATGTTTCTGCTGGAAGGCTGGAGGAGCAATTAACACACT 424  
QY 373 ATATATCCAGAGCATGACAGAGATGTTTCTGCTGGAAGGCTGGAGGAGCAATTAACACACT 432  
DB 425 ATATATCCAGAGCATGACAGAGATGTTTCTGCTGGAAGGCTGGAGGAGCAATTAACACACT 484  
QY 433 GCAAACGGGCTCT 446  
DB 485 GCAAACGGGCTCT 498

RESULT 2  
US-09-023-655-1390  
; Sequence 1390, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO. 1390:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 490 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: G396163  
US-09-023-655-1390

Query Match 65.5%; Score 418; DB 4; Length 490;

Best Local Similarity 100.0%; Pred. No. 1.4e-208;  
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 CTGCTGAGCCATGCTGAGGGGAATCAACCTTTCAGAGCCCTGACCGAAGTTTAA 88  
Db 1 CTGCTGAGCATGCTGAGGGGAATCAACCTTTCAGAGCCCTGACCGAAGTTTAA 60  
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QY 149 CTGAGAGATCTTCCGATGTCAGATGGATGGGCAAGGAGCAGAGCGACACACAT 208  
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RESULT 3  
US-09-929-945-3  
; Sequence 3, Application US/09929945  
; Patent No. 6642026  
; GENERAL INFORMATION:  
; APPLICANT: Stegmann, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Olexandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
; FILE REFERENCE: FIBROBLAST GROWTH FACTOR 155  
; CURRENT FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 468  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-929-945-3

Query Match 63.9%; Score 408; DB 4; Length 468;  
Best Local Similarity 100.0%; Pred. No. 2.4e-203;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATGCTGAGGGGAATACCACTTTCAGAGCCCTGACCGAAGTTTAACTGCTCCA 98  
Db 1 ATGCTGAGGGGAATACCACTTTCAGAGCCCTGACCGAAGTTTAACTGCTCCA 60  
QY 99 GGGAAATTACAAAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCACTTCTGAGGATC 158  
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QY 159 CTTCGGATGGCAAGTGGATGGGCAAGGGACAGGACGACGACCAATTCAGCTGCAG 218  
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QY 339 CTGGAAGGCTGGAGGAGAACCAATTAACACCTATATATATCAAGAGCATGCGAGAG 398  
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Db 361 AATGTTGTTGTTGGCTTCAAGAGAAATGGAGCTGCAAGCGGTCT 408

RESULT 4  
US-08-793-900-1  
; Sequence 1, Application US/08793900  
; Patent No. 6143518  
; GENERAL INFORMATION:  
; APPLICANT: CAMERON, Beatrice  
; APPLICANT: CROUZET, Joel  
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF RECOMBINANT  
; TITLE OF INVENTION: PROTEINS, PLASMIDS AND MODIFIED CELLS  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, Mailstop 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/793,900  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR95/01178  
; FILING DATE: 14-SEP-1995  
; APPLICATION NUMBER: FR 94/11049  
; FILING DATE: 16-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky Esq., Martin F.  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: ST94069-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3816  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8501 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: cDNA  
US-08-793-900-1

Query Match 63.9%; Score 408; DB 3; Length 8501;  
Best Local Similarity 100.0%; Pred. No. 2.7e-203;  
Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATGCTGAGGGGAATACCACTTTCAGAGCCCTGACCGAAGTTTAACTGCTCCA 98  
Db 108 ATGCTGAGGGGAATACCACTTTCAGAGCCCTGACCGAAGTTTAACTGCTCCA 167  
QY 99 GGGAAATTACAAAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCACTTCTGAGGATC 158  
Db 168 GGGAAATTACAAAGAGCCCAAACTCTCTACTGTAGCAACGGGGCCACTTCTGAGGATC 227  
QY 159 CTTCGGATGGCAAGTGGATGGGCAAGGGACAGGACGACGACCAATTCAGCTGCAG 218  
Db 228 CTTCGGATGGCAAGTGGATGGGCAAGGGACAGGACGACGACCAATTCAGCTGCAG 287  
QY 219 CTCAGTGGCAAGCTGGGGAGGTGTATATAAGAGTACCGAGCTGGCCAGTACTTG 278  
Db 288 CTCAGTGGCAAGCTGGGGAGGTGTATATAAGAGTACCGAGCTGGCCAGTACTTG 347  
QY 279 GCGATGACACCGACGGGCTTTTATACGGCTCAGACACCAATAGGAATGTTGTTTC 338  
Db 348 GCGATGACACCGACGGGCTTTTATACGGCTCAGACACCAATAGGAATGTTGTTTC 407

QY 339 CTGGAAGGCTGGAGGAGAACCACTTACACACCTTATATCCAGAGCATGCGAGAG 398  
DB 408 CTGGAAGGCTGGAGGAGAACCACTTACACACCTTATATCCAGAGCATGCGAGAG 467  
QY 399 AATTGGTTTGTGGCTTCAAGAGAAATGGAGCTGCAACCGCGTCT 446  
DB 468 AATTGGTTTGTGGCTTCAAGAGAAATGGAGCTGCAACCGCGTCT 515

RESULT 5  
5175147-1  
; Patent No. 5175147  
; APPLICANT: FOLKMAN, MOSES J.; KATO, KOICHI  
; TITLE OF INVENTION: ACID-RESISTANT FGF COMPOSITION AND METHOD  
; OF TREATING ULцерATING DISEASES OF THE GASTROINTESTINAL TRACT  
; NUMBER OF SEQUENCES: 19  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/382,263  
; FILING DATE: 20-JUL-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 234,966  
; FILING DATE: 19-AUG-1988  
; SEQ ID NO:1:  
; LENGTH: 454  
5175147-1

Query Match 29.2%; Score 186; DB 6; Length 454;  
Best Local Similarity 99.3%; Pred. No. 2.2e-87;  
Matches 286; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 159 CTTCGGATGGCAGACGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 218  
DB 92 CTTCGGATGGCAGACGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 151  
QY 219 CTCAGTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 278  
DB 152 CTCAGTCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 211  
QY 279 GCCATGGACACCGCGGCTTTTATACGCTCAGACACCAATGAGGAGTGTTC 338  
DB 212 GCATGGACACCGCGGCTTTTATACGCTCAGACACCAATGAGGAGTGTTC 271  
QY 339 CTGGAAGGCTGGAGGAGAACCACTTACACACCTTATATCCAGAGCATGCGAGAG 398  
DB 272 CTGGAAGGCTGGAGGAGAACCACTTACACACCTTATATCCAGAGCATGCGAGAG 331  
QY 399 AATTGGTTTGTGGCTTCAAGAGAAATGGAGCTGCAACCGCGTCT 446  
DB 332 AATTGGTTTGTGGCTTCAAGAGAAATGGAGCTGCAACCGCGTCT 379

RESULT 6  
5514566-3  
; Patent No. 5514566  
; APPLICANT: FIDDES, JOHN C.; ABRAHAM, JUDITH A.  
; TITLE OF INVENTION: METHODS OF PRODUCING RECOMBINANT  
; FIBROBLASTS GROWTH FACTORS  
; NUMBER OF SEQUENCES: 21  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/417,022  
; FILING DATE: 05-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 809,163  
; FILING DATE: 16-DEC-1985  
; APPLICATION NUMBER: 775,521  
; FILING DATE: 12-SEP-1985  
; SEQ ID NO:3:  
; LENGTH: 197  
5514566-3

Query Match 27.0%; Score 172; DB 6; Length 197;  
Best Local Similarity 100.0%; Pred. No. 4.4e-80;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 36 GCCATGGCTGAAGGGGAAATCACACCTTTCACAGCCCTGACCGAGAGTTTAATCTGCCT 95  
DB 7 GCCATGGCTGAAGGGGAAATCACACCTTTCACAGCCCTGACCGAGAGTTTAATCTGCCT 66

QY 96 CCAGGGAAATTCAGAGAACGCCAACTCTCTTACTGTAGCAACGGGGGCCACTTCTCTGAGG 155  
DB 67 CCAGGGAAATTCAGAGAACGCCAACTCTCTTACTGTAGCAACGGGGGCCACTTCTCTGAGG 126  
QY 156 ATCTCTTCGGAGTGGACAGTGGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 207  
DB 127 ATCTCTTCGGAGTGGACAGTGGATGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 178

RESULT 7  
5437995-1  
; Patent No. 5437995  
; APPLICANT: ICHIMORI, YUZO; KONDO, KOICHI; IGARASHI, KOICHI;  
; SENDO, MASAHARU  
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AGAINST AN ACIDIC  
; FGF PROTEIN AND HYBRIDOMA FOR ITS PRODUCTION  
; NUMBER OF SEQUENCES: 3  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/26,257  
; FILING DATE: 04-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 588,343  
; FILING DATE: 26-SEP-1990  
; SEQ ID NO:1:  
; LENGTH: 450  
5437995-1

Query Match 18.5%; Score 118; DB 6; Length 450;  
Best Local Similarity 100.0%; Pred. No. 7.4e-52;  
Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 285 GACACCGACGGGCTTTTATACGCTCAGACACCAATGAGGAGTGTTCCTGAA 344  
DB 216 GACACCGACGGGCTTTTATACGCTCAGACACCAATGAGGAGTGTTCCTGAA 275  
QY 345 AGCGTGGAGGAGAACCACTTACACACCTTATATCCAGAGCATGCGAGAGAGTT 402  
DB 276 AGCGTGGAGGAGAACCACTTACACACCTTATATCCAGAGCATGCGAGAGAGTT 333

RESULT 8  
US-09-030-613-14  
; Sequence 14, Application US/09030613  
; Patent No. 6083706  
; GENERAL INFORMATION:  
; APPLICANT: Florckiewicz, Robert Z.  
; TITLE OF INVENTION: INHIBITORS OF LEADERLESS PROTEIN EXPORT  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,613  
; FILING DATE: 25-FEB-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6083706tenburg Ph.D., Carol  
; REGISTRATION NUMBER: 39,317  
; REFERENCE/DOCKET NUMBER: 760100.418C1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 454 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-030-613-14

Query Match 12.1%; Score 77; DB 3; Length 454;  
Best Local Similarity 100.0%; Pred. No. 1.9e-30;  
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 282 ATGGACACCGCGGCTTTTATACGGCTCAGACACCAAAATGAGGAATGTTGTTCTG 341  
DB 246 ATGGACACCGCGGCTTTTATACGGCTCAGACACCAAAATGAGGAATGTTGTTCTG 305  
QY 342 GAAAGGCTGGAGAGAA 358  
DB 306 GAAAGGCTGGAGAGAA 322

RESULT 9  
US-09-451-905-14  
; Sequence 14, Application US/09451905  
; Patent No. 6306613  
; GENERAL INFORMATION:  
; APPLICANT: Robert Z. Florkiewicz  
; APPLICANT: Andrew Baird  
; APPLICANT: Dale E. Warnock  
; TITLE OF INVENTION: MODULATORS OF LEADERLESS PROTEIN EXPORT  
; FILE REFERENCE: 200124.402C4  
; CURRENT FILING DATE: 1999-12-01  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 454  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-451-905-14

Query Match 12.1%; Score 77; DB 4; Length 454;  
Best Local Similarity 100.0%; Pred. No. 1.9e-30;  
Matches 77; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 282 ATGGACACCGCGGCTTTTATACGGCTCAGACACCAAAATGAGGAATGTTGTTCTG 341  
DB 246 ATGGACACCGCGGCTTTTATACGGCTCAGACACCAAAATGAGGAATGTTGTTCTG 305  
QY 342 GAAAGGCTGGAGAGAA 358  
DB 306 GAAAGGCTGGAGAGAA 322

RESULT 10  
US-09-929-945-1  
; Sequence 1, Application US/09929945  
; Patent No. 6642026  
; GENERAL INFORMATION:  
; APPLICANT: Stegmann, Thomas  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT  
; FILE REFERENCE: CUGEN.008A  
; CURRENT APPLICATION NUMBER: US/09/929,945  
; CURRENT FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 630  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized sequence for human acidic  
; OTHER INFORMATION: Fibroblast Growth Factor (155 amino acids) using  
; OTHER INFORMATION: preferred codons for E. coli  
; NAME/KEY: CDS  
; LOCATION: (122)...(590)  
US-09-929-945-1

Query Match 4.1%; Score 26; DB 4; Length 630;  
Best Local Similarity 100.0%; Pred. No. 0.00086;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 39 ATGGCTGAAGGGGAATCACCACCTT 64  
DB 122 ATGGCTGAAGGGGAATCACCACCTT 147

RESULT 11  
5514566-1  
; Patent No. 5514566  
; APPLICANT: FIDES, JOHN C.; ABRAHAM, JUDITH A.  
; TITLE OF INVENTION: METHODS OF PRODUCING RECOMBINANT  
; FIBROBLAST GROWTH FACTORS  
; NUMBER OF SEQUENCES: 21  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/417,022  
; FILING DATE: 05-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 809,163  
; FILING DATE: 16-DEC-1985  
; APPLICATION NUMBER: 775,521  
; FILING DATE: 12-SEP-1985  
; SEQ ID NO: 1  
; LENGTH: 270  
5514566-1

Query Match 3.8%; Score 24; DB 6; Length 270;  
Best Local Similarity 100.0%; Pred. No. 0.0092;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 26 CAGCTGTGAGCCATGCGCTGAAG 49  
DB 9 CAGCTGTGAGCCATGCGCTGAAG 32

RESULT 12  
US-08-023-757-8  
; Sequence 8, Application US/08023757  
; Patent No. 5302702  
; GENERAL INFORMATION:  
; APPLICANT: Seddon Dr., Andrew P.  
; APPLICANT: Bohlen Dr., Peter  
; APPLICANT: Gluzman Dr., Yakov  
; TITLE OF INVENTION: Chimeric Fibroblast Growth Factors  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: American Cyanamid Company  
; STREET: 1937 West Main Street, P. O. Box 60  
; CITY: Stamford,  
; STATE: CT  
; COUNTRY: USA  
; ZIP: 06904-0060  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/023,757  
; FILING DATE: 26-FEB-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/615,202  
; FILING DATE: 23-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Tsevdos Dr., Estelle J.  
; REGISTRATION NUMBER: 31,145  
; REFERENCE/DOCKET NUMBER: 31,219-00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 203-321-2756  
; TELEFAX: 203-321-2971  
; TELEX: 710-474-4059  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 44 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)

/ HYPOTHETICAL: NO  
/ ANTI-SENSE: NO  
/ ORIGINAL SOURCE:  
/ ORGANISM: HUMAN  
US-08-023-757-8

Query Match 3.6%; Score 23; DB 1; Length 44;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATGGCTGAAGGGGAATCACCAC 61  
DB 9 ATGGCTGAAGGGGAATCACCAC 31

RESULT 13

US-08-177-502-8  
; Sequence 8, Application US/08177502  
; Patent No. 5371206

/ GENERAL INFORMATION:

/ APPLICANT: Seddon Dr., Andrew P.  
/ APPLICANT: Bohlen Dr., Peter  
/ APPLICANT: Gluzman Dr., Yakov  
/ TITLE OF INVENTION: Chimeric Fibroblast Growth Factors  
/ NUMBER OF SEQUENCES: 8  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: American Cyanamid Company  
/ STREET: 1937 West Main Street, P. O. Box 60  
/ CITY: Stamford,  
/ STATE: CT  
/ COUNTRY: USA  
/ ZIP: 06904-0060

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent in Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/177,502  
/ FILING DATE: 05-JAN-1994  
/ CLASSIFICATION: 435  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/023,757  
/ FILING DATE: 26-FEB-1993  
/ APPLICATION NUMBER: US/07/615,202  
/ FILING DATE: 23-NOV-1990  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Tsevdos Dr., Estelle J.  
/ REGISTRATION NUMBER: 31,145  
/ REFERENCE/DOCKET NUMBER: 31,219-00  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 203-321-2756  
/ TELEFAX: 203-321-2971  
/ TELEX: 710-474-4059

/ INFORMATION FOR SEQ ID NO: 8:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 44 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: DNA (genomic)

/ HYPOTHETICAL: NO

/ ANTI-SENSE: NO

/ ORIGINAL SOURCE:

/ ORGANISM: HUMAN

US-08-177-502-8

Query Match 3.6%; Score 23; DB 1; Length 44;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATGGCTGAAGGGGAATCACCAC 61  
DB 9 ATGGCTGAAGGGGAATCACCAC 31

RESULT 14

US-08-054-650A-2

; Sequence 2, Application US/08054650A

/ Patent No. 5387673

/ GENERAL INFORMATION:

/ APPLICANT: Seddon, Andrew P.  
/ APPLICANT: Bohlen, Peter  
/ TITLE OF INVENTION: Active Fragments of Fibroblast Growth  
/ TITLE OF INVENTION: Factor  
/ NUMBER OF SEQUENCES: 5  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Anne M. Rosenblum  
/ STREET: 163 Delaware Avenue, Suite 212  
/ CITY: Delmar  
/ STATE: New York  
/ COUNTRY: USA  
/ ZIP: 12054

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent in Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/054,650A  
/ FILING DATE: 26-APR-1993  
/ CLASSIFICATION: 530  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Tsevdos, Estelle J.  
/ REGISTRATION NUMBER: 31145  
/ REFERENCE/DOCKET NUMBER: 31309-01  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (518)475-0611  
/ TELEFAX: (518)475-0619  
/ INFORMATION FOR SEQ ID NO: 2:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 44 base pairs  
/ TYPE: nucleic acid  
/ STRANDEDNESS: double  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: cDNA

US-08-054-650A-2

Query Match 3.6%; Score 23; DB 1; Length 44;

Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 ATGGCTGAAGGGGAATCACCAC 61

DB 9 ATGGCTGAAGGGGAATCACCAC 31

RESULT 15

US-08-383-621-11

; Sequence 11, Application US/08383621

; Patent No. 5951972

/ GENERAL INFORMATION:

/ APPLICANT: Daley, Michael J.  
/ APPLICANT: Buckwalter, Brian L.  
/ APPLICANT: Cady, Susan M.  
/ APPLICANT: Shieh, Hong-Ming  
/ APPLICANT: Bohlen, Peter  
/ APPLICANT: Seddon, Andrew P.  
/ TITLE OF INVENTION: Stabilization Of Somatotropins And Other  
/ TITLE OF INVENTION: Proteins By Modification Of Cysteine Residues  
/ NUMBER OF SEQUENCES: 11  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: Dr. Estelle J. Tsevdos  
/ STREET: 1937 West Main Street, P.O. Box 60  
/ CITY: Stamford  
/ STATE: Connecticut  
/ COUNTRY: U.S.A.  
/ ZIP: 06904-0060

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patent in Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/383,621  
/ FILING DATE: 06-FEB-1995  
/ CLASSIFICATION: 514  
/ PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/766,142  
FILING DATE: 25-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Teevdos, Estelle J.  
REGISTRATION NUMBER: 31,145  
REFERENCE/DOCKET NUMBER: 31,278-01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 203-321-2756  
TELEFAX: 203-321-2971  
TELEX: 203-710-474-4059  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-383-621-11

Query Match 3.6%; Score 23; DB 2; Length 44;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 23; Conservative 0; Mismatches 0; Gaps 0;

QY 39 ATGCTGAAGGGGAATCCAC 61  
|||||  
Db 9 ATGCTGAAGGGGAATCCAC 31  
|||||

Search completed: August 24, 2004, 23:07:01  
Job time : 87 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 21:00:28 ; Search time 482 Seconds  
(without alignments)  
6501.952 Million cell updates/sec

Title: US-10-022-554A-3

Perfect score: 638

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Gapop 60.0 , Gapext 60.0

Searched: 3228839 seqs, 245606551 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6457678

Minimum DB seq length: 0

Maximum DB seq length: 200000000

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11: /cgn2\_6/ptodata/1/pubna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/1/pubna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/1/pubna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/1/pubna/US10D\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/1/pubna/US10\_NEW\_PUB.seq.\*

18: /cgn2\_6/ptodata/1/pubna/US60\_NEW\_PUB.seq.\*  
19: /cgn2\_6/ptodata/1/pubna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	434	68.0	638	10	US-09-902-460-3	Sequence 3, Appli
2	434	68.0	4087	14	US-10-044-090-225	Sequence 225, Appl
3	418	65.5	490	15	US-10-388-410-8	Sequence 8, Appli
4	418	65.5	490	17	US-10-641-643-1390	Sequence 1390, Ap
5	408	63.9	468	9	US-09-929-918-3	Sequence 3, Appli
6	408	63.9	468	9	US-09-929-945-3	Sequence 3, Appli
7	408	63.9	468	15	US-10-280-864-3	Sequence 3, Appli
8	408	63.9	468	17	US-10-649-480-3	Sequence 3, Appli
C 9	195	30.6	580	9	US-09-864-761-13391	Sequence 13391, A
C 10	187	29.3	187	9	US-09-864-761-29943	Sequence 29943, A
11	147	23.0	478	16	US-10-116-275-235	Sequence 235, App
12	135	21.2	3658	12	US-09-968-007A-133	Sequence 133, App
13	135	21.2	3658	12	US-09-968-007A-440	Sequence 440, App
14	26	4.1	65	10	US-09-908-975-28515	Sequence 28515, A
15	26	4.1	630	9	US-09-929-918-1	Sequence 1, Appli
16	26	4.1	630	9	US-09-929-945-1	Sequence 1, Appli
17	26	4.1	630	15	US-10-280-864-1	Sequence 1, Appli
18	26	4.1	630	17	US-10-649-480-1	Sequence 1, Appli
19	26	4.1	990	9	US-09-929-918-10	Sequence 10, Appl
20	22	3.4	29	10	US-09-847-936B-13	Sequence 13, Appl
C 21	21	3.3	28	10	US-09-847-936B-12	Sequence 12, Appl
22	21	3.3	630	9	US-09-929-918-4	Sequence 4, Appli
23	21	3.3	630	9	US-09-929-918-6	Sequence 6, Appli
24	21	3.3	630	9	US-09-929-945-4	Sequence 4, Appli
25	21	3.3	630	9	US-09-929-945-6	Sequence 6, Appli
26	21	3.3	630	15	US-10-280-864-4	Sequence 4, Appli
27	21	3.3	630	17	US-10-649-480-4	Sequence 4, Appli
28	21	3.3	630	17	US-10-649-480-6	Sequence 6, Appli
29	21	3.3	630	17	US-10-649-480-6	Sequence 6, Appli
30	20	3.1	20	10	US-09-981-803-19	Sequence 19, Appl
31	20	3.1	20	15	US-10-104-025-1	Sequence 1, Appli
C 32	20	3.1	637	13	US-10-027-632-188645	Sequence 188645, A
C 33	20	3.1	637	13	US-10-027-632-188646	Sequence 188646, A
C 34	20	3.1	637	16	US-10-027-632-188645	Sequence 188645, A
C 35	20	3.1	637	16	US-10-027-632-188646	Sequence 188646, A
C 36	19	3.0	581	9	US-09-864-761-9138	Sequence 9138, Ap
C 37	19	3.0	1231	17	US-10-437-963-22726	Sequence 22726, A
C 38	19	3.0	2121	17	US-10-437-963-64740	Sequence 64740, A
C 39	19	3.0	2715	9	US-09-764-870-65	Sequence 65, Appl
40	19	3.0	2715	15	US-10-125-540-65	Sequence 473, App
C 41	19	3.0	4270	15	US-10-000-256A-84	Sequence 182, App
42	19	3.0	4715	13	US-10-296-115-473	Sequence 182, App
43	19	3.0	5111	13	US-10-342-887-182	Sequence 182, App
44	19	3.0	5111	13	US-10-172-118-182	Sequence 1, Appli
C 45	19	3.0	2256646	17	US-10-470-565-1	Sequence 1, Appli

# ALIGNMENTS

RESULT 1  
US-09-902-460-3  
; Sequence 3, Application US/09902460  
; Publication No. US2003040042A1  
; GENERAL INFORMATION:  
; APPLICANT: FIDDES, J.C.  
; ABRAM, J.D.  
; TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH  
; FACTOR ANALOG  
; NUMBER OF SEQUENCE: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FORESTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018



COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICANT: US/09/902.460  
FILING DATE: 09-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/098.628  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Lehnhardt, Susan K  
REGISTRATION NUMBER: 33,943  
REFERENCE/DOCKET NUMBER: 21900-20089.10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-813-5600  
TELEFAX: 650-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 638 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
MOLECULE TYPE: linear  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 91...555  
OTHER INFORMATION:  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-902-460-3

Query Match 68.0%; Score 434; DB 10; Length 638;  
Best Local Similarity 100.0%; Pred. No. 3.9e-215;  
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GGGCCCAAGCAGCAGCTGCTGAGCCATGCTGAGCGGGAATACCAACCTTCACAGCC 72  
Db 65 GGGCCCAAGCAGCAGCTGCTGAGCCATGCTGAGCGGGAATACCAACCTTCACAGCC 124  
QY 73 TGACCGAGAGTTTAACTGCTGCTGAGCGGGAATACCAACCTTCACAGCT 132  
Db 125 TGACCGAGAGTTTAACTGCTGCTGAGCGGGAATACCAACCTTCACAGCT 184  
QY 133 GCAACGGGGCCCACTTCTGAGGATCTTCCGATGCGACAGTGGGAGGTTATATAA 192  
Db 185 GCAACGGGGCCCACTTCTGAGGATCTTCCGATGCGACAGTGGGAGGTTATATAA 244  
QY 193 GGAGCCACGACAGCATTCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 252  
Db 245 GGAGCCACGACAGCATTCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 304  
QY 253 AGAGTACCGAGACTGGCCAGTACTTGGCCATGACACCGAGGCTTTTATACGGCTCAC 312  
Db 305 AGAGTACCGAGACTGGCCAGTACTTGGCCATGACACCGAGGCTTTTATACGGCTCAC 364  
QY 313 AGACACCAATGAGGAATGTTGTTCTGGAAAGCTTGGAGGAAACCATTAACACCT 372  
Db 365 AGACACCAATGAGGAATGTTGTTCTGGAAAGCTTGGAGGAAACCATTAACACCT 424  
QY 373 ATATATCCAAAGCAGCATGACAGAGAAATTTGTTGCTGAGGCTTCAAGAGATGGAGCT 432  
Db 425 ATATATCCAAAGCAGCATGACAGAGAAATTTGTTGCTGAGGCTTCAAGAGATGGAGCT 484  
QY 433 GCAACGGGGTCTCT 446  
Db 485 GCAACGGGGTCTCT 498

RESULT 2  
US-10-044-090-225  
Sequence 225, Application US/10044090  
Publication No. US20020137081A1  
GENERAL INFORMATION:  
APPLICANT: Olga Bandman  
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION  
FILE REFERENCE: PA-0028 US

CURRENT APPLICATION NUMBER: US/10/044,090  
CURRENT FILING DATE: 2002-01-09  
NUMBER OF SEQ ID NOS: 850  
SOFTWARE: PERL Program  
SEQ ID NO 225  
LENGTH: 4087  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20020137081A1 336376.2  
US-10-044-090-225

Query Match 68.0%; Score 434; DB 14; Length 4087;  
Best Local Similarity 100.0%; Pred. No. 3.4e-215;  
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GGGCCCAAGCAGCAGCTGCTGAGCCATGCTGAGCGGGAATACCAACCTTCACAGCC 72  
Db 480 GGGCCCAAGCAGCAGCTGCTGAGCCATGCTGAGCGGGAATACCAACCTTCACAGCC 539  
QY 73 TGACCGAGAGTTTAACTGCTGCTGAGCGGGAATACCAACCTTCACAGCT 132  
Db 540 TGACCGAGAGTTTAACTGCTGCTGAGCGGGAATACCAACCTTCACAGCT 599  
QY 133 GCAACGGGGCCCACTTCTGAGGATCTTCCGATGCGACAGTGGGAGGTTATATAA 192  
Db 600 GCAACGGGGCCCACTTCTGAGGATCTTCCGATGCGACAGTGGGAGGTTATATAA 659  
QY 193 GGAGCCACGACAGCATTCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 252  
Db 660 GGAGCCACGACAGCATTCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 719  
QY 253 AGAGTACCGAGACTGGCCAGTACTTGGCCATGACACCGAGGCTTTTATACGGCTCAC 312  
Db 720 AGAGTACCGAGACTGGCCAGTACTTGGCCATGACACCGAGGCTTTTATACGGCTCAC 779  
QY 313 AGACACCAATGAGGAATGTTGTTCTGGAAAGCTTGGAGGAAACCATTAACACCT 372  
Db 780 AGACACCAATGAGGAATGTTGTTCTGGAAAGCTTGGAGGAAACCATTAACACCT 839  
QY 373 ATATATCCAAAGCAGCATGACAGAGAAATTTGTTGCTGAGGCTTCAAGAGATGGAGCT 432  
Db 840 ATATATCCAAAGCAGCATGACAGAGAAATTTGTTGCTGAGGCTTCAAGAGATGGAGCT 899  
QY 433 GCAACGGGGTCTCT 446  
Db 900 GCAACGGGGTCTCT 913

RESULT 3  
US-10-388-410-8  
Sequence 8, Application US/10388410  
Publication No. US20030157548A1  
GENERAL INFORMATION:  
APPLICANT: NAWA, HIROYUKI  
APPLICANT: TAKAHASHI, HITOSHI  
APPLICANT: IRTANI, SHUJI  
TITLE OF INVENTION: METHOD FOR DIAGNOSING SCHIZOPHRENIA USING OBJECTIVE INDICES  
FILE REFERENCE: 235447USOCONT  
CURRENT APPLICATION NUMBER: US/10/388,410  
CURRENT FILING DATE: 2003-03-17  
PRIOR APPLICATION NUMBER: US 09/723,224  
PRIOR FILING DATE: 2000-11-28  
PRIOR APPLICATION NUMBER: JP 2000-061775  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 8  
LENGTH: 490  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-388-410-8

Query Match 65.5%; Score 418; DB 15; Length 490;  
Best Local Similarity 100.0%; Pred. No. 8.4e-207;  
Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 29 CTGCTGAGCCATGGCTGAGGGAATACCAACCTTCACAGCCCTTCACGAGAGTTTAA 88

Db	1	CTGCTGAGCATGCTGAGGGGAAATCACCACTTCTACAGCCTGTACCGCAGAGCTTTAA	60
QY	89	TCTGCTCCAGGGAATTACAAGAGCCCAAACTCTCTACTGTAGCAACCGGGGCGCACTT	148
Db	61	TCTGCTCTCCAGGGAATTACAAGAGCCCAAACTCTCTACTGTAGCAACCGGGGCGCACTT	120
QY	149	CCTCAGGATGCTTCCGGATGGCAAGTGGATGGCAAGAGGACAGAGCGACACGACAT	208
Db	121	CCTGAGGATGCTTCCGGATGGCAAGTGGATGGCAAGAGGACAGAGCGACACGACAT	180
QY	209	TCAGCTGCAGCTCAGTGCAGGAAAGCGTGGCGGAGGTGTATATAAGAGTACCGAGACTGG	268
Db	181	TCAGCTGCAGCTCAGTGCAGGAAAGCGTGGCGGAGGTGTATATAAGAGTACCGAGACTGG	240
QY	269	CCAGTACTTGGCGATGGACACGAGCGGCTTTTATACGGCTCACAGACCAAAATGAGGA	328
Db	241	CCAGTACTTGGCGATGGACACGAGCGGCTTTTATACGGCTCACAGACCAAAATGAGGA	300
QY	329	ATGTTTGTCTCGAAGCGCTGGAGGAGAAACATTACAACACTATATATCCACAGCA	388
Db	301	ATGTTTGTCTCGAAGCGCTGGAGGAGAAACATTACAACACTATATATCCACAGCA	360
QY	389	TGCAGAGAAGAAATGGTTTGTGGCTTCAAGAGAATGGGAGCTGCAAAACGGGTCCT	446
Db	361	TGCAGAGAAGAAATGGTTTGTGGCTTCAAGAGAATGGGAGCTGCAAAACGGGTCCT	418

## RESULT 4

RESULT 4  
US-10-641-1390  
; Sequence 1390, Application US/10641643  
; Publication No. US20040077003A1  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; Susan G. Stuart  
; Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
; GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/641,643  
; FILING DATE: 14-Aug-2003  
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1390:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 490 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g396163  
SEQUENCE DESCRIPTION: SEQ ID NO: 1390 :  
10-641-643-1390

Query Match 65.5%; Score 418; DB 17; Length 490;  
Best Local Similarity 100.0%; Pred. No. 8.4e-207;

RESULT 7

US-10-280-864-3

: Sequence 3, Application US/10280864

: Publication NO. US20030054492A1

: GENERAL INFORMATION:

: APPLICANT: Stegmann, Thomas

: APPLICANT: Kordyum, Vitaliy A.

: APPLICANT: Chernykh, Svitlana I.

: APPLICANT: Slavchenko, Iryna Yu.

: APPLICANT: Vozirandov, Aleksandr

TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT

TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155

FILE REFERENCE: CVGENG.008A

CURRENT APPLICATION NUMBER: US/10/280.864

	Query Match	63.9%	Score 408	DB 17	Length 468	
	Best Local Similarity	100.0%	Pred. NO. 1.3e-201			
	Matches 408	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	39	ATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAAGATTAACTGCCTCCA	98			
DB	1	ATGGCTGAAGGGGAAATCACCACCTTCACAGCCCTGACCGAAGATTAACTGCCTCCA	60			
QY	99	GGGAAATTACAGAGCCCAAACTCTCTACTGTAGACGGGGGCCACTTCTTGAGGATC	159			

61 GGGATTACAGAGCCGAACTCTCTACTGTGATGACAGGGGGCCACTCTCTGAGATC 120

159 CTTCCGGATGGCAGCTGGATGGGACAAGGGGACAGAGGACGACACATTCAGCTCGAG 218

121 CTTCCGGATGGCAGCTGGATGGGACAAGGGGACAGAGGACGACACATTCAGCTCGAG 180

219 CTCATCTCGGAAGCGTGGGGAGGTGTATATAAGACTACGAGACTTGGCCAGTACTTG 278

181 CTCAGTGGGAAAGCGTGGGGAGGTGTATATAAGGTACCGACTGTGCCCTACTCTG 240

279 GCATPAGACACCGACGGGCTTTTATACGGCTCTACAGACCAAAATGAGGAATGTTCTC 338

241 GCCATPAGACACCGACGGGCTTTTATACGGCTCTACAGACCAAAATGAGGAATGTTCTC 300

339 CTGGAAAGGCTGGAGAGAAACATTACACACTTATATCCAAAGCATSCAGAGAG 398

301 CTGGAAAGGCTGGAGAGAAACATTACACACTTATATCCAAAGCATSCAGAGAG 360

399 AATTGGTTTGTGGCTCTCAAGAGAATGGAGCTGCGAAACGGCGTCT 446

361 AATTGGTTTGTGGCTCTCAAGAGAATGGAGCTGCGAAACGGCGTCT 408

RESULT 9

US-09-864-761-13391/c

; Sequence 13391, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aecmica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

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/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263.6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 13391
/ LENGTH: 580
/ TYPE: DNA

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; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 29943  
; LENGTH: 187  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC010489.4  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.1  
; OTHER INFORMATION: EST HUMAN HIT: AI590078.1, EVALUE 1.00e-101  
; OTHER INFORMATION: SWISSPROT HIT: P05230, EVALUE 6.00e-29  
; OTHER INFORMATION: NT HIT: GI11416219, EVALUE 1.00e-101  
US-09-864-761-29943

Query Match 29.3%; Score 187; DB 9; Length 187;  
Best Local Similarity 100.0%; Pred. No. 1.3e-86;  
Matches 187; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ASCGAGCTGCTGAGCCATGCTGAGGGGAATCACCACCTTCACAGCCCTGACCGAG 80  
Db |||||||  
QY 187 AGCAGAGCTGCTGAGCCATGCTGAGGGGAATCACCACCTTCACAGCCCTGACCGAG 128  
Db |||||||  
QY 81 AAGTTTAAATCTGCTCAGGGAATTTACAGAGCCCAAACTCTCTACTGTAGCAACGGG 140  
Db |||||||  
QY 141 GGCACACTTCTGAGATCTCTCCGATGGCAGTGGATGGGACAGGGACAGGAGCGAC 200  
Db |||||||  
QY 67 GGCACACTTCTGAGATCTCTCCGATGGCAGTGGATGGGACAGGGACAGGAGCGAC 8  
Db |||||||  
QY 201 CAGCACA 207  
Db |||||||  
QY 7 CAGCACA 1

RESULT 11  
US-10-116-275-235  
; Sequence 235, Application US/10116275  
; Publication No. US20030211476A1  
; GENERAL INFORMATION:  
; APPLICANT: Eln Pharmacental Technology  
; APPLICANT: O'Mahony, Daniel J.  
; APPLICANT: Brayden, David  
; APPLICANT: Byrne, Daragh  
; APPLICANT: Lambkin, Imelda  
; APPLICANT: Higgins, Lisa  
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods  
and  
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors  
; FILE REFERENCE: E1067/20087  
; CURRENT APPLICATION NUMBER: US/10/116.275  
; CURRENT FILING DATE: 2002-10-04  
; SOFTWARE: PatentIn version 3.1  
; NUMBER OF SEQ ID NOS: 349  
; SEQ ID NO 235  
; LENGTH: 478  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-116-275-235

Query Match 23.0%; Score 147; DB 16; Length 478;  
Best Local Similarity 100.0%; Pred. No. 7.6e-66;  
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCGCCACAGCAGCAGCTGAGCAGTGGCTGAGGGGAATTTACAGAGCCCAAACTCTCTACTGTA 132  
Db |||||||  
QY 332 GCGCCACAGCAGCAGCTGAGCAGTGGCTGAGGGGAATTTACAGAGCCCAAACTCTCTACTGTA 391  
Db |||||||  
QY 73 TGACCCGAGAAGTTTAACTCTGCTCCAGGGAATTTACAGAGCCCAAACTCTCTACTGTA 132  
Db |||||||  
QY 392 TGACCCGAGAAGTTTAACTCTGCTCCAGGGAATTTACAGAGCCCAAACTCTCTACTGTA 451  
Db |||||||  
QY 133 GCACAGGGGGCCACTCTCGAGGATCC 159  
Db |||||||  
QY 452 GCACAGGGGGCCACTCTCTGAGGATCC 478  
Db |||||||

RESULT 12  
US-09-968-007A-133  
; Sequence 133, Application US/09968007A

Publication No. US20040115625A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner, Reinhard  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature  
; TITLE OF INVENTION: Gene Sets  
; FILE REFERENCE: 689290-71  
; CURRENT APPLICATION NUMBER: US/09/968.007A  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,172  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,173  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,278  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,294  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,295  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,316  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 1001  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 440  
; LENGTH: 3658  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-968-007A-440

Query Match 21.2%; Score 135; DB 12; Length 3658;  
Best Local Similarity 100.0%; Pred. No. 1.1e-59;  
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 312 CAGACACCAATGAGGAATTTTGTCTCGAAAGGCTTGGAGGAGAACCACTTACACACC 371  
Db |||||||  
QY 304 CAGACACCAATGAGGAATTTTGTCTCGAAAGGCTTGGAGGAGAACCACTTACACACC 363  
Db |||||||  
QY 372 TATATATCAAGAAGCATGCGAGAGAGATTTGTTTGTGGCTTCAAGACATCGAGCC 431  
Db |||||||  
QY 364 TATATATCAAGAAGCATGCGAGAGAGATTTGTTTGTGGCTTCAAGACATCGAGCC 423  
Db |||||||  
QY 432 TCGAACGCGGCTCT 446  
Db |||||||  
QY 424 TCGAACGCGGCTCT 438  
Db |||||||

RESULT 13  
US-09-968-007A-440  
; Sequence 440, Application US/09968007A  
; Publication No. US20040115625A1  
; GENERAL INFORMATION:  
; APPLICANT: Ebner, Reinhard  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signature  
; TITLE OF INVENTION: Gene Sets  
; FILE REFERENCE: 689290-71  
; CURRENT APPLICATION NUMBER: US/09/968.007A  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,172  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,173  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,278  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,294  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,295  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: US/60/237,316  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 1001  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 440  
; LENGTH: 3658  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-968-007A-440

Query Match 21.2%; Score 135; DB 12; Length 3658;

Best Local Similarity 100.0%; Pred. No. 1.1e-59;  
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 312 CAGACACCAATAGGAATGTTTCTCTGGAAGGCTGAGAGAACCAATTACACACC 371  
DB 304 CAGACACCAATAGGAATGTTTCTCTGGAAGGCTGAGAGAACCAATTACACACC 363  
QY 372 TATATATCCAGACGATGACAGAGAAATGTTTCTCTGGAAGGCTGAGAGAACCAATTACACACC 431  
DB 364 TATATATCCAGACGATGACAGAGAAATGTTTCTCTGGAAGGCTGAGAGAACCAATTACACACC 423  
QY 432 TGCACACGGGCTCT 446  
DB 424 TGCACACGGGCTCT 438

#### RESULT 14

US-09-908-975-28515  
; Sequence 28515, Application US/09908975  
; Publication No. US20030165843A1  
; GENERAL INFORMATION:  
; APPLICANT: SHOSHAN, Avi  
; APPLICANT: WASSERMAN, Alon  
; APPLICANT: MINTZ, Eli  
; APPLICANT: MINTZ, Liat  
; APPLICANT: FAIGLER, Simchon  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND  
; SPICE VARIANTS  
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME  
; FILE REFERENCE: 36688-0005  
; CURRENT APPLICATION NUMBER: US/09/908,975  
; CURRENT FILING DATE: 2001-07-20  
; PRIOR APPLICATION NUMBER: US 60/287,724  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/221,607  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 32337  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 28515  
; LENGTH: 65  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-908-975-28515

Query Match 4.1%; Score 26; DB 10; Length 65;  
Best Local Similarity 100.0%; Pred. No. 0.0078;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 267 GCCCAGTACTTGGCCATGACACCGA 292  
DB 21 GCCCAGTACTTGGCCATGACACCGA 46

#### RESULT 15

US-09-929-918-1  
; Sequence 1, Application US/09929918  
; Patent No. US2002090678A1  
; GENERAL INFORMATION:  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svitlana I.  
; APPLICANT: Slavchenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: PHASE-DEPENDENT SUPER PRODUCTION OF  
; FILE REFERENCE: PHAGE.006A  
; CURRENT APPLICATION NUMBER: US/09/929,918  
; CURRENT FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: 09/318,288  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 630  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: This sequence was chemically synthesized based  
; upon the amino acid sequence of human acidic  
; OTHER INFORMATION: fibroblast growth factor (155 amino acids) using

; OTHER INFORMATION: codons which are used in highly expressed proteins from E.  
coli.  
; NAME/KEY: CDS  
; LOCATION: (122)...(590)  
US-09-929-918-1  
Query Match 4.1%; Score 26; DB 9; Length 630;  
Best Local Similarity 100.0%; Pred. No. 0.0065;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 39 ATGCTGAAGGGGAAATCACCACCTT 64  
DB 122 ATGCTGAAGGGGAAATCACCACCTT 147  
Search completed: August 24, 2004, 23:15:18  
Job time : 485 secs

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: August 24, 2004, 20:50:43 ; Search time 2845 Seconds  
(without alignments)  
6696.686 Million cell updates/sec

Title: US-10-022-554A-3  
Perfect score: 638  
Sequence: 1 gaattcgggaacgcgcaca.....cctgaatttgaagcaactt 638

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Database : ESI:

1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estma:\*  
5: em\_estov:\*  
6: em\_estol:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_ges\_hum:\*  
18: em\_ges\_inv:\*  
19: em\_ges\_pln:\*  
20: em\_ges\_vrt:\*  
21: em\_ges\_fun:\*  
22: em\_ges\_mam:\*  
23: em\_ges\_mus:\*  
24: em\_ges\_pro:\*  
25: em\_ges\_rod:\*  
26: em\_ges\_phg:\*  
27: em\_ges\_vrl:\*  
28: gb\_ges1:\*  
29: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,

Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bto.llnl.gov/bbrp/image/image.html](http://www-bto.llnl.gov/bbrp/image/image.html)  
Insert Length: 736 Std Error: 0.00  
Seq primer: -400bp from Gibco  
High quality sequence stop: 455.

## FEATURES

Result No.	Score	Query			ID	Description	
		Match	Length	DB			
C	1	434	68.0	534	9	A1590078	
	2	434	68.0	821	12	B1598390	B1590078 tms8c01.x
	3	434	68.0	1014	12	BM809005	A1598390 603250094
	4	434	68.0	1057	13	BK067949	BM809005 AGENCOURT
	5	434	68.0	1173	13	BX444567	BK067949 AGENCOURT
	6	321	50.3	832	12	B1869731	BX444567 BX444567
	7	317	49.7	522	14	CD701495	B1869731 603393620
	8	296	46.8	714	12	BK706412	CD701495 EST18019
	9	292	45.8	461	10	BF956865	BK706412 602669744
	10	282	44.2	678	12	BF956865	BF956865 RCI-NN023
C	11	279	43.7	611	13	B1753845	BF956865 RCI-NN023
	12	277	43.4	678	12	B1753845	B1753845 603027526
	13	277	43.4	678	12	B1753845	B1753845 603027526
	14	205	32.4	750	13	BUE27243	BUE40197 AGENCOURT
	15	188	29.5	570	12	B1868848	BUE40197 AGENCOURT
	16	147	23.0	364	9	A1864448	BX488304 DXFZP686G
	17	144	22.6	415	9	A1083919	BUE27243 UI-H-FGO-
	18	116	18.2	386	10	BF958824	AA015793 ze30a12.r
	19	113	17.7	701	12	BM995210	B1598882 603247981
	20	111	17.4	424	14	H23109	A1864448 w153c07.x
C	21	109	17.1	352	12	BG700150	A1083919 qf26c07.x
	22	101	15.8	472	9	A1077609	BM995210 UI-H-ED0-
	23	81	12.7	255	14	R58184	H23109 ym51f12.r1
	24	77	12.1	689	12	B1550213	BG700150 602679586
	25	75	11.8	364	14	R14113	A1077609 oy26d02.s
	26	74	11.6	503	10	BF442355	R58184 F9465 Fetal
	27	72	11.3	458	9	AA594274	B1550213 603192318
	28	72	11.3	458	14	R54255	R14113 yf69e06.r1
	29	72	11.3	482	10	AW207545	BF442355 259038 MA
	30	72	11.3	588	12	BQ060606	AA594274 nl90q01.s
C	31	71	11.1	364	9	A1359575	R54255 yq74af06.r1
	32	70	11.0	498	13	BX501193	BQ060606 UI-H-Eil-
	33	61	9.6	525	29	CG556846	AW207545 UI-H-Bil-
	34	59	9.2	242	29	CG556846	BQ060606 UI-H-Eil-
	35	59	9.2	309	29	CG556846	A1359575 qy32c08.x
	36	59	9.2	313	29	CG4965943	BX501193 DXFZP779H
	37	59	9.2	344	13	BX349996	CG556846 OST195476
	38	59	9.2	344	13	BX349996	CG556846 OST195476
	39	59	9.2	344	13	BX349996	CG556846 OST195476
	40	59	9.2	344	13	BX349996	CG556846 OST195476
C	41	59	9.2	359	13	BX320462	CG4965943 OST37278
	42	59	9.2	368	13	BX230638	CG605210 OST281652
	43	59	9.2	373	13	BX235986	BV349996 BY349996
	44	59	9.2	403	29	CG613113	CG605210 OST281652
	45	59	9.2	418	13	BX327122	BV349996 BY349996
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							BX320462 BY302462
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							BY230638 BY230638
							BY235986 BY235986

## RESULT 1

AI590078/c	AI590078	AI590078.1	GI:4599126	EST.	Human sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	NCBI/NINDS-CGAP site <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	linear	EST 21-APR-1999
LOCUS	AI590078	AI590078	AI590078.1	EST.	Human sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	NCBI/NINDS-CGAP site <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	linear	EST 21-APR-1999
DEFINITION	AI590078	AI590078	AI590078.1	EST.	Human sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	NCBI/NINDS-CGAP site <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	linear	EST 21-APR-1999
DESCRIPTION	AI590078	AI590078	AI590078.1	EST.	Human sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	NCBI/NINDS-CGAP site <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	linear	EST 21-APR-1999
ACCESSION	AI590078	AI590078	AI590078.1	EST.	Human sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	NCBI/NINDS-CGAP site <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	linear	EST 21-APR-1999
VERSION	AI590078	AI590078	AI590078.1	EST.	Human sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	NCBI/NINDS-CGAP site <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	linear	EST 21-APR-1999
KEYWORDS	AI590078	AI590078	AI590078.1	EST.	Human sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	NCBI/NINDS-CGAP site <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	linear	EST 21-APR-1999
SOURCE	AI590078	AI590078	AI590078.1	EST.	Human sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	NCBI/NINDS-CGAP site <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	linear	EST 21-APR-1999
ORGANISM	AI590078	AI590078	AI590078.1	EST.	Human sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	NCBI/NINDS-CGAP site <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	linear	EST 21-APR-1999
REFERENCE	AI590078	AI590078	AI590078.1	EST.	Human sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	NCBI/NINDS-CGAP site <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	linear	EST 21-APR-1999
AUTHORS	AI590078	AI590078	AI590078.1	EST.	Human sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	NCBI/NINDS-CGAP site <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	linear	EST 21-APR-1999
TITLE	AI590078	AI590078	AI590078.1	EST.	Human sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	NCBI/NINDS-CGAP site <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	linear	EST 21-APR-1999
JOURNAL	AI590078	AI590078	AI590078.1	EST.	Human sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	NCBI/NINDS-CGAP site <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	linear	EST 21-APR-1999
COMMENT	AI590078	AI590078	AI590078.1	EST.	Human sapiens (human)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	NCBI/NINDS-CGAP site <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	linear	EST 21-APR-1999



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 821)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
 Toshiyuki and Piero Carninci (RIKEN)  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM1764 row: k column: 23  
 High quality sequence stop: 777.  
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 (GTCGAG); Oligo-dT primed using primer  
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 insert size 2.3 kb and normalized to 10^5. This is a  
 primary library enriched for full-length clones and  
 constructed using the Cap-trapper method (Carninci, in  
 preparation). Library constructed by M. Brownstein  
 (NIH/NHGRI, National Institutes of Health). Note: this is  
 a NIH MGC Library."

# ORIGIN

Query Match 68.0%; Score 434; DB 12; Length 821;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-211;  
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GGGCCACAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCC 72  
 DB 124 GGGCCACAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCC 183  
 QY 73 TGAACGAGAGTTTAATCTGCTCCAGGGAATTACAGAGCCCAAACTCTCTACTGTA 132  
 DB 184 TGAACGAGAGTTTAATCTGCTCCAGGGAATTACAGAGCCCAAACTCTCTACTGTA 243  
 QY 133 GCAACGGGGGCACTTCTGAGGATCTTCGGGATGCGACATGGATGGGCAAGGGACA 192  
 DB 244 GCAACGGGGGCACTTCTGAGGATCTTCGGGATGCGACATGGATGGGCAAGGGACA 303  
 QY 193 GGAGCCACCAACCAATTCAGCTCAGCTCAGTGGGAAAGCTGGGGAGGTGTATATAA 252  
 DB 304 GGAGCCACCAACCAATTCAGCTCAGCTCAGTGGGAAAGCTGGGGAGGTGTATATAA 363  
 QY 253 AGATGACGAGCTGGCCAGTACTTGCCATGAGCAACCGAGGGCTTTTATACGGCTCAC 312  
 DB 364 AGATGACGAGCTGGCCAGTACTTGCCATGAGCAACCGAGGGCTTTTATACGGCTCAC 423  
 QY 313 AGACACCAATGAGAAATGTTGTTCTGAAAGCTGGGAGCAACCAATTCACACCT 372  
 DB 424 AGACACCAATGAGAAATGTTGTTCTGAAAGCTGGGAGCAACCAATTCACACCT 483  
 QY 373 ATATATCCAGAGCATGACAGAGAATTTGGTTTGTGGCTTCAGAGAATGGAGCT 432  
 DB 484 ATATATCCAGAGCATGACAGAGAATTTGGTTTGTGGCTTCAGAGAATGGAGCT 543  
 QY 433 GCAACGGGGTCTT 446  
 DB 544 GCAACGGGGTCTT 557

RESULT 3  
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DEFINITION AGNCOURT\_6617747 NIH\_MGC\_124 Homo sapiens cDNA clone IMAGE:5734445  
 5', mRNA sequence.  
 ACCESSION BM809005  
 VERSION BM809005.1 GI:19125828  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Invitrogen  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM12739 row: m column: 06  
 High quality sequence stop: 637.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
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 /clone="IMAGE:5734445"  
 /tissue\_type="hippocampus"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_MGC\_124"  
 /notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: EcoRV  
 (destroyed); Site 2: NotI; RNA source male hippocampus,  
 age 27. Library is oligo-dT primed and directionally  
 cloned (EcoRV site is destroyed upon cloning). Average  
 insert size 1.4 kb, insert size range 0.9-4 kb. Library is  
 normalized and enriched for full-length clones and was  
 constructed by C. Gruber (Invitrogen). Research Genetics  
 tracking code 012."

# ORIGIN

Query Match 68.0%; Score 434; DB 12; Length 1014;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-211;  
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GGGCCACAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCC 72  
 DB 157 GGGCCACAGCAGCAGCTGCTGAGCCATGGCTGAAGGGGAAATCACCACCTTCACAGCC 216  
 QY 73 TGAACGAGAGTTTAATCTGCTCCAGGGAATTACAGAGCCCAAACTCTCTACTGTA 132  
 DB 217 TGAACGAGAGTTTAATCTGCTCCAGGGAATTACAGAGCCCAAACTCTCTACTGTA 276  
 QY 133 GCAACGGGGGCACTTCTGAGGATCTTCGGGATGCGACATGGATGGGCAAGGGACA 192  
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 DB 337 GGAGCCACCAACCAATTCAGCTCAGCTCAGTGGGAAAGCTGGGGAGGTGTATATAA 396  
 QY 253 AGATGACGAGCTGGCCAGTACTTGCCATGAGCAACCGAGGGCTTTTATACGGCTCAC 312  
 DB 397 AGATGACGAGCTGGCCAGTACTTGCCATGAGCAACCGAGGGCTTTTATACGGCTCAC 456  
 QY 313 AGACACCAATGAGAAATGTTGTTCTGAAAGCTGGGAGCAACCAATTCACACCT 372  
 DB 457 AGACACCAATGAGAAATGTTGTTCTGAAAGCTGGGAGCAACCAATTCACACCT 516  
 QY 373 ATATATCCAGAGCATGACAGAGAATTTGGTTTGTGGCTTCAGAGAATGGAGCT 432  
 DB 517 ATATATCCAGAGCATGACAGAGAATTTGGTTTGTGGCTTCAGAGAATGGAGCT 496  
 QY 433 GCAACGGGGTCTT 446  
 DB 577 GCAACGGGGTCTT 590

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 AGENCOURT\_6792377 NIH\_MGC\_121 Homo sapiens cDNA clone IMAGE:5768943  
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 ACCESSION  
 BQ067949  
 VERSION  
 BQ067949.1 GI:19896995  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NIH-MGC http://mgi.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue procurement: Life Technologies, Inc.  
 cDNA library Preparation: Life Technologies, Inc.  
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM12829 row: j column: 16  
 High quality sequence stop: 470.  
 Location/Qualifiers  
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 /clone="IMAGE:5768943"  
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 /clone\_lib="NIH\_MGC\_121"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: EcoRV (destroyed); RNA source anonymous pool of 3  
 fetal brains, female age 20 weeks, female age 24 weeks,  
 and male age 26 weeks. Library is oligo-dT primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.7 kb, insert size range  
 0.7-3.5 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 017. Note:  
 this is a NIH\_MGC Library."

ORIGIN  
 Query Match 68.0%; Score 434; DB 13; Length 1057;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-211;  
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 GCGCCACAGCAGCAGCTGCTGAGCCATGCTGAGGGGAAATCAACACCTTCACAGCCC 72  
 DB 115 GCGCCACAGCAGCAGCTGCTGAGCCATGCTGAGGGGAAATCAACACCTTCACAGCCC 174  
 QY 73 TGACCGAGAGTTTAATCTGCTCCAGGGAATTACAGAGCCCAAACTCTCTACTGTA 132  
 DB 175 TGACCGAGAGTTTAATCTGCTCCAGGGAATTACAGAGCCCAAACTCTCTACTGTA 234  
 QY 133 GCACGGGGGGCCACTTCCTCGAGATCTTCGGATGGCAGTGGGAGGAGGAGGAGCA 192  
 DB 235 GCACGGGGGGCCACTTCCTCGAGATCTTCGGATGGCAGTGGGAGGAGGAGGAGCA 294  
 QY 193 GGAGGACACAGCAGATTCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 252  
 DB 295 GGAGGACACAGCAGATTCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 354  
 QY 253 AGAGTACCGAGATGGCCAGTACTTGCCATGGACACCGACGGGCTTTTATACGGCTCAC 312  
 DB 355 AGAGTACCGAGATGGCCAGTACTTGCCATGGACACCGACGGGCTTTTATACGGCTCAC 414  
 QY 313 AGACACCAATGAGAGTGTGTGCTCGAAGGCTGAGAGGAGGAGGAGGAGGAGGAGG 372  
 DB 415 AGACACCAATGAGAGTGTGTGCTCGAAGGCTGAGAGGAGGAGGAGGAGGAGGAGG 474  
 QY 373 ATATATCCAAAGAGCATGCAAGAGAAATTGGTTTGTGGCTTCAAGAGAGTGGAGCT 432  
 DB 475 ATATATCCAAAGAGCATGCAAGAGAAATTGGTTTGTGGCTTCAAGAGAGTGGAGCT 534

QY 433 GCACCAAGCGGCTCT 446  
 DB 535 GCACCAAGCGGCTCT 548  
 RESULT 5  
 BX444567  
 LOCUS  
 DEFINITION  
 BX444567 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone  
 CSODN003YP16 5-PRIME, mRNA sequence.  
 ACCESSION  
 BX444567  
 VERSION  
 BX444567.1 GI:30780253  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 1173)  
 Li.W.B., Gruber,C., Jessee,J. and Polayes,D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 3201.r For  
 more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CSODN003DH08QPlccluster=3201.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
 Faraday Avenue Genoscope sequence ID : CSODN003DH08QPl.  
 Location/Qualifiers  
 1. .1173  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="CSODN003YP16"  
 /tissue\_type="ADULT BRAIN"  
 /dev\_stage="adult"  
 /clone\_lib="Homo sapiens ADULT BRAIN"  
 /note="Organ: brain; Vector: pCMVSPORT\_6; 1st strand cDNA  
 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-strand cDNA was digested with Not I and  
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6  
 vector. Library was not normalized."

ORIGIN  
 Query Match 68.0%; Score 434; DB 13; Length 1173;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-211;  
 Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 GCGCCACAGCAGCAGCTGCTGAGCCATGCTGAGGGGAAATCAACACCTTCACAGCCC 72  
 DB 142 GCGCCACAGCAGCAGCTGCTGAGCCATGCTGAGGGGAAATCAACACCTTCACAGCCC 201  
 QY 73 TGACCGAGAGTTTAATCTGCTCCAGGGAATTACAGAGCCCAAACTCTCTACTGTA 132  
 DB 202 TGACCGAGAGTTTAATCTGCTCCAGGGAATTACAGAGCCCAAACTCTCTACTGTA 261  
 QY 133 GCACGGGGGGCCACTTCCTCGAGATCTTCGGATGGCAGTGGGAGGAGGAGGAGCA 192  
 DB 262 GCACGGGGGGCCACTTCCTCGAGATCTTCGGATGGCAGTGGGAGGAGGAGGAGCA 321  
 QY 193 GGAGGACACAGCAGATTCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 252  
 DB 322 GGAGGACACAGCAGATTCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 381  
 QY 253 AGAGTACCGAGATGGCCAGTACTTGCCATGGACACCGACGGGCTTTTATACGGCTCAC 312  
 DB 382 AGAGTACCGAGATGGCCAGTACTTGCCATGGACACCGACGGGCTTTTATACGGCTCAC 441  
 QY 313 AGACACCAATGAGAGTGTGTGCTCGAAGGCTGAGAGGAGGAGGAGGAGGAGGAGG 372  
 DB 442 AGACACCAATGAGAGTGTGTGCTCGAAGGCTGAGAGGAGGAGGAGGAGGAGGAGG 501  
 QY 373 ATATATCCAAAGAGCATGCAAGAGAAATTGGTTTGTGGCTTCAAGAGAGTGGAGCT 432

Db 502 ATATATCCAGAGCATGACAGAGAGAGTGTGTTGTTGGCTCAAGAGAGATGGAGGCT 561

QY 433 GCAAGCGGCTCT 446

Db 562 GCAAGCGGCTCT 575

RESULT 6

LOCUS B1869731 832 bp mRNA linear EST 11-OCT-2001

DEFINITION 603393620F1 NIH\_MGC\_90 Homo sapiens cDNA clone IMAGE:5403677 5', mRNA sequence.

ACCESSION B1869731

VERSION B1869731.1 GI:16043404

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 832)

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE NIH-MGC http://mgc.nci.nih.gov/.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgep@rs-mail.nih.gov

Tissue procurement: ATCC

cDNA library preparation: Life Technologies, Inc.

cDNA library arrayed by: The I.M.A.G.E. Consortium (LMNL)

Cloning strategy: In-cyte Genomics, Inc.

Cloning distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: L1AM12029 row: 9 column: 06

High quality sequence stop: 829.

FEATURES

source

1. 832

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5403677"

/tissue\_type="adenocarcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_90"

/note="Organ; liver; Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 50.3%; Score 321; DB 12; Length 832;

Best Local Similarity 100.0%; Pred. No. 2.6e-153;

Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GGGCCACACAGCAGCAGCTGTCGATGCGATGCTGAAGGGGAAATACACACCTTCACAGCC 72

Db 54 GCGCCACACAGCAGCAGCTGTCGATGCGATGCTGAAGGGGAAATACACACCTTCACAGCC 113

QY 73 TGACCGAGAGTTTAACTGCTTCGAGGAGTTTACAGAGCCGCTCTCTACTGTA 132

Db 114 TCACCGAGAGTTTAACTGCTTCGAGGAGTTTACAGAGCCGCTCTCTACTGTA 173

QY 133 GCAACGGGGGCCACTCTCGAGGATCTTCGGATGCGACAGTGGAGGAGGATATATA 192

Db 174 GCAACGGGGGCCACTCTCGAGGATCTTCGGATGCGACAGTGGAGGAGGATATATA 233

QY 193 GAGGACACGACATTCAGTGTGACGTCAGTGTGCGAAAGCGTGGGGAGGATATATA 252

Db 234 GAGGACACGACATTCAGTGTGACGTCAGTGTGCGAAAGCGTGGGGAGGATATATA 293

QY 253 AGAGTACCGAGCTGGCCAGTACTTGGCCATGACACCGAGGCTTTTATACGGCTC 312

Db 294 AGAGTACCGAGCTGGCCAGTACTTGGCCATGACACCGAGGCTTTTATACGGCTC 353

QY 313 AGACACCAATGAGGATGTT 333

Db 354 AGACACCAATGAGGATGTT 374

RESULT 7

LOCUS CD701495 522 bp mRNA linear EST 25-JUN-2003

DEFINITION EST18019 human nasopharynx Homo sapiens cDNA, mRNA sequence.

ACCESSION CD701495

VERSION CD701495.1 GI:32232125

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 522)

AUTHORS Liu, X.-O., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-X., Pan, Z.-G. and Zeng, Y.-X.

TITLE Transcriptional Gene Expression Profile of Human Nasopharynx

JOURNAL Unpublished (2003)

COMMENT Contact: Yixin Zeng

Cancer Center

651 Dongfeng Road East, Guangzhou 510060, China

Tel: 86-1380-9770-743

Fax: 86-20-8775-4506

Email: yxzeng@gzsums.edu.cn.

Location/Qualifiers

1. 522

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue\_type="normal nasopharynx"

/clone\_lib="human nasopharynx"

/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 49.7%; Score 317; DB 14; Length 522;

Best Local Similarity 100.0%; Pred. No. 2.7e-151;

Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCGCCACACAGCAGCAGCTGTCGAGCCATGCGTGAAGGGGAAATACACACCTTCACAGCC 72

Db 206 GCGCCACACAGCAGCAGCTGTCGAGCCATGCGTGAAGGGGAAATACACACCTTCACAGCC 265

QY 73 TGACCGAGAGTTTAACTGCTTCACAGGAAATACACAGAGCCCAACTCTCTACTGTA 132

Db 266 TGACCGAGAGTTTAACTGCTTCACAGGAAATACACAGAGCCCAACTCTCTACTGTA 325

QY 133 GCACGGGGGCCACTCTCGAGGATCTTCGGATGCGACAGTGGAGGAGGATATATA 192

Db 326 GCACGGGGGCCACTCTCGAGGATCTTCGGATGCGACAGTGGAGGAGGATATATA 385

QY 193 GAGGACACGACATTCAGCTGCGAGCTCAGTGGGAAAGCGTGGGGAGGATATATA 252

Db 386 GAGGACACGACATTCAGCTGCGAGCTCAGTGGGAAAGCGTGGGGAGGATATATA 445

QY 253 AGAGTACCGAGCTGGCCAGTACTTGGCCATGACACCGAGGCTTTTATACGGCTC 312

Db 446 AGAGTACCGAGCTGGCCAGTACTTGGCCATGACACCGAGGCTTTTATACGGCTC 505

QY 313 AGACACCAATGAGGAA 329

Db 506 AGACACCAATGAGGAA 522

RESULT 8

LOCUS BG706412 714 bp mRNA linear EST 07-MAY-2001

DEFINITION 602669744F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:4792378 5', mRNA sequence.

ACCESSION BG706412

VERSION BG706412.1 GI:13981735

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 714)

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
COMMENT

Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cchapb-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shizaki  
Toshiyuki and Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM10670 row: h column: 11  
High quality sequence stop: 710.  
Location/Qualifiers

FEATURES

source  
1. .714  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4792378"  
/tissue\_type="hypothalamus"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC 96"  
/note="Organ: brain; Vector: pBluescriptR (modified  
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI  
(gtcag); Oligo-dT primed using primer  
5'-TTTTTTTTTTTTTTVN-3', size-selected for average  
insert size 2.3 kb and normalized to ROT 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NIH/NHGRI, National Institutes of Health). Note: this is  
a NIH\_MGC Library."

ORIGIN

Query Match 46.4%; Score 296; DB 12; Length 714;  
Best Local Similarity 99.7%; Pred. No. 1.7e-140;  
Matches 346; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 100 GGAATTACAGAAAGCCAACTCTCTACTGTAGCAACGCGGCGCCACTCTCTGAGGATCC 159  
DB 210 GGATATACAGAAAGCCAACTCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 269  
QY 160 TTCCGGATGGCAAGTGGATGGGCAAGGAGGACAGGAGGAGGAGGAGGAGGAGGAGGAGG 219  
DB 270 TTCCGGATGGCAAGTGGATGGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 329  
QY 220 TCAGTCGGAAAGCGTGGGGAGGAGTGTATATAGAGTACCGAGACTGGCCAGTACTTGG 279  
DB 330 TCAGTCGGAAAGCGTGGGGAGGAGTGTATATAGAGTACCGAGACTGGCCAGTACTTGA 389  
QY 280 CCATGAGACACGAGCGGCTTTTATACGGCTTCACAGACCAAAATGAGGAATGTTTTC 339  
DB 390 CCATGAGACACGAGCGGCTTTTATACGGCTTCACAGACCAAAATGAGGAATGTTTTC 449  
QY 340 TGGAAAGCGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 399  
DB 450 TGGAAAGCGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 509  
QY 400 ATTGGTTTGTGGCTTCAAGAAGATGGGAGCTGCAACGCGGTCT 446  
DB 510 ATTGGTTTGTGGCTTCAAGAAGATGGGAGCTGCAACGCGGTCT 556

RESULT 9

BF956865  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

BF956865 461 bp mRNA linear EST 22-JAN-2001  
RCL-NN0233-221100-011-h12 NN0233 Homo sapiens cDNA, mRNA sequence.  
BF956865  
BF956865.1 GI:12374140  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 461)  
Dias Neto P., Garcia Correa R., Verjovski-Almeida S., Briones M.R.,  
Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F.,  
Goldman G.H., Carvalho A.F., Matsukuma A., Baia G.S., Simpson D.H.,  
Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V.,

O'Hare M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and  
Simpson A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
PUBMED  
10737800

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gechtml2.pl?cl=RC1&t2=RC1-NN0233-  
221100-011-h12&t3=2000-11-22&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 11  
High quality sequence stop: 461.  
Location/Qualifiers

FEATURES

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1. .461  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="NN0233"  
/note="Organ: nervous normal; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (O.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

ORIGIN

Query Match 45.8%; Score 292; DB 10; Length 461;  
Best Local Similarity 100.0%; Pred. No. 1.8e-138;  
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 155 GATCCTTCCTCGGATGGCAGTGGATGGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 214  
DB 44 GATCCTTCCTCGGATGGCAGTGGATGGGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 103  
QY 215 GCAGCTCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 274  
DB 104 GCAGCTCAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 163  
QY 275 CTGCGCATGAGACCGGCGCTTTTATACGGCTTCACAGACCAAAATGAGGAATGTTT 334  
DB 164 CTGCGCATGAGACCGGCGCTTTTATACGGCTTCACAGACCAAAATGAGGAATGTTT 223  
QY 335 GTTCTCGGAAAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 394  
DB 224 GTTCTCGGAAAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 283  
QY 395 GAAGAAATGGTTTGTGGCTTCAAGAAGATGGGAGCTGCAACGCGGTCT 446  
DB 284 GAAGAAATGGTTTGTGGCTTCAAGAAGATGGGAGCTGCAACGCGGTCT 335

RESULT 10

BF953845  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

BF953845 878 bp mRNA linear EST 25-SEP-2001  
603027526F1 NIH\_MGC\_114 Homo sapiens cDNA clone IMAGE:5197783 5',  
mRNA sequence.  
BF953845  
BF953845.1 GI:15745423  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 878)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cga@rs-nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11495 row: d column: 08  
High quality sequence stop: 703.  
Location/Qualifiers  
1. .878

FEATURES  
source

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5197783"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_114"  
/note="Organ: brain; Vector: pCMV-Sport6; Site: 1: NoCI; Site: 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb. Insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 44.2%; Score 282; DB 12; Length 878;  
Best Local Similarity 100.0%; Pred. No. 2.8e-133;  
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 CTCCTCTACTGTGACACGGGGCCACTTCCTGAGATCTTCGGATCGACAGTGGAT 179  
Db 199 CTCCTCTACTGTGACACGGGGCCACTTCCTGAGATCTTCGGATCGACAGTGGAT 258  
QY 180 GGCACAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 239  
Db 259 GGCACAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 318  
QY 240 GAGGTGTATATTAAGAGTACCGACGACGACGACGACGACGACGACGACGACGAC 299  
Db 319 GAGGTGTATATTAAGAGTACCGACGACGACGACGACGACGACGACGACGACGACGAC 378  
QY 300 TTATACGGCTACACGACCAATAGGAGATGTTGTTCTGAAAGGCTGGAGGACAC 359  
Db 379 TTATACGGCTACACGACCAATAGGAGATGTTGTTCTGAAAGGCTGGAGGACAC 438  
QY 360 CATTACACACCTATATTCACAGACGATGACAGAGAT 401  
Db 439 CATTACACACCTATATTCACAGACGATGACAGAGAT 480

RESULT 11

BUB40197  
LOCUS BUB40197 611 bp mRNA linear EST 16-OCT-2002  
DEFINITION AGENCOURT\_8964623 NIH\_MGC\_42 Homo sapiens cDNA clone IMAGE:6379201  
5', mRNA sequence.  
ACCESSION BUB40197  
VERSION BUB40197.1 GI:24024592  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 611)  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@rs-nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov  
Plate: LLCW2565 row: n column: 02  
High quality sequence stop: 610.  
Location/Qualifiers  
1. .611  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6379201"  
/tissue\_type="epithelioid carcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_42"  
/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 43.7%; Score 279; DB 13; Length 611;  
Best Local Similarity 100.0%; Pred. No. 9e-132;  
Matches 279; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 GGCACAGTGCATGGACAGGACGACGACGACGACGACGACGACGACGACGACGAC 227  
Db 141 GGCACAGTGCATGGACAGGACGACGACGACGACGACGACGACGACGACGACGAC 200  
QY 228 GAAACGTGGGGAGGTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGAC 287  
Db 201 GAAACGTGGGGAGGTGTATATAAAGAGTACCGAGACTGGCCAGTACTTGGCCATGGAC 260  
QY 288 ACCGACGGGCTTTATACGGCTCCACAGACCAATAGGAGATGTTGTTCTGGAAAGG 347  
Db 261 ACCGACGGGCTTTATACGGCTCCACAGACCAATAGGAGATGTTGTTCTGGAAAGG 320  
QY 348 CTGGAGGAGAACCTTACCAACCTATATATCAAGAGCAGTGCAGAGAGAAATTTGTTT 407  
Db 321 CTGGAGGAGAACCTTACCAACCTATATATCAAGAGCAGTGCAGAGAGAAATTTGTTT 380  
QY 408 GTTGCCCTCAAGAGAAATGGAGCTGCACACGGGCTCT 446  
Db 381 GTTGCCCTCAAGAGAAATGGAGCTGCACACGGGCTCT 419

RESULT 12

BX488304  
LOCUS BX488304 420 bp mRNA linear EST 04-SEP-2003  
DEFINITION DKFZp686G16269 r1.686 (synonym: hlcc3) Homo sapiens cDNA clone  
5', mRNA sequence.  
ACCESSION BX488304  
VERSION BX488304.1 GI:31953759  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 420)  
REFERENCE Bloembergen, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.  
EST (Bloembergen, H., Boecher, M., Mewes, H.W., Weil, B., Amid, C., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MIPS  
MIPS  
Ingoltsedter Landstr. 1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;  
sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.  
No 5' sequence available.  
This clone (DKFZp686G16269) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers

FEATURES

Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGTCACCTC. The cell lines was provided by Dr. James Martin from University of Iowa.

TAG: TISSUE=Enchondroma cell line (Mix of EN1 and EN2)  
TAG\_LIB=UI-H-FG0  
TAG\_SEQ=CCGTCACCTC

ORIGIN

Query Match 32.4%; Score 207; DB 13; Length 750;  
Best Local Similarity 100.0%; Pred. No. 8.9e-95;  
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 240 GAGGTGTATTAAGAGTACGAGACTGGCCACTTGGCCATGACACCGACGGGCTT 299  
DB 675 GAGGTGTATTAAGAGTACGAGACTGGCCACTTGGCCATGACACCGACGGGCTT 616  
QY 300 TTATACGGCTCACACACCAATGAGGAATGTTTCTTGGAAAGGCTGGAGGAGAAC 359  
DB 615 TTATACGGCTCACACACCAATGAGGAATGTTTCTTGGAAAGGCTGGAGGAGAAC 556  
QY 360 CATTAACACCTTATATATCCAGAGCATGACAGAGAAATGTTTGTGGCTCTCAAG 419  
DB 555 CATTAACACCTTATATATCCAGAGCATGACAGAGAAATGTTTGTGGCTCTCAAG 496  
QY 420 AAGATGGGAGCTGCACAAAGCGGTCT 446  
DB 495 AAGATGGGAGCTGCACAAAGCGGTCT 469

RESULT 14

AA015793 460 bp mRNA linear EST 29-NOV-1996  
LOCUS ze30a12.r1 Soares retina N2B4HR Homo sapiens cDNA clone  
DEFINITION IMAGE:360478 5' similar to gb:M13361 HEPARIN-BINDING GROWTH FACTOR  
PRECURSOR 1 (HUMAN); mRNA sequence.

ACCESSION AA015793  
VERSION AA015793.1 GI:1476960  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 460)  
AUTHORS Hillier, L., Clark, N., Dubuque, T., Ellington, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, I., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Woldmann, P. and Wilson, R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.wustl.edu  
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert length: 3013 Std Error: 0.00  
Seq primer: -28M13 rev2 from Amersham  
High quality sequence stop: 372.  
Location/Qualifiers  
1. .460  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="CDB:1277023"  
/db\_xref="taxon:9606"  
/clone="IMAGE:360478"  
/sex="male"  
/tissue\_type="retina"  
/dev\_stage="55 year old"  
/lab\_host="DH10B (ampicillin resistant)"

FEATURES

source

1. .460  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="CDB:1277023"  
/db\_xref="taxon:9606"  
/clone="IMAGE:360478"  
/sex="male"  
/tissue\_type="retina"  
/dev\_stage="55 year old"  
/lab\_host="DH10B (ampicillin resistant)"

1. .420  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp586G16263"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Vector: pTriplex2; Site\_1: SfiIA; Site\_2: SfiIB;  
cDNA-collection"

ORIGIN

Query Match 43.4%; Score 277; DB 13; Length 420;  
Best Local Similarity 100.0%; Pred. No. 8.9e-131;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 GCGCCCAACAGCAGAGCTGCTGAGCCATGGCTGAAGGGGAATACACCTTCACAGCC 72  
DB 144 GCGCCCAACAGCAGAGCTGCTGAGCCATGGCTGAAGGGGAATACACCTTCACAGCC 203  
QY 73 TGACCGAAGTTTATCTGCTCGAGGGAATACAGAGCCCAAACTCTCTACTGTA 132  
DB 204 TGACCGAAGTTTATCTGCTCGAGGGAATACAGAGCCCAAACTCTCTACTGTA 263  
QY 133 GCACGGGGGCCACTCTCTGAGGATCTCTCCGGATGGCAGCTGGATGGGACAGGACA 192  
DB 264 GCACGGGGGCCACTCTCTGAGGATCTCTCCGGATGGCAGCTGGATGGGACAGGACA 323  
QY 193 GAGCGCAGCAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 252  
DB 324 GAGCGCAGCAGCAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 383  
QY 253 AGATGACGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 289  
DB 384 AGATGACGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 420

RESULT 13

BU627243/c 750 bp mRNA linear EST 23-SEP-2002  
LOCUS UI-H-FG0-bct-n-05-0-UI.s1 NCI CGAP EN1\_2 Homo sapiens cDNA clone  
DEFINITION UI-H-FG0-bct-n-05-0-UI 3', mRNA sequence.

ACCESSION BU627243  
VERSION BU627243.1 GI:23293457  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 750)  
AUTHORS NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapb-remail.nih.gov  
Tissue Procurement: James Martin  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu  
Seq primer: M13 FORWARD  
POLYA=Yes.  
Location/Qualifiers  
1. .750  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FG0-bct-n-05-0-UI"  
/tissue\_type="Enchondroma cell line"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP EN1\_2"  
/note="Organ: Bone; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; NCI CGAP EN1\_2 is a cDNA library containing the following tissue(s): Enchondroma cell line (2 cell lines). The library was constructed according to Bonaldo, Lennon and

FEATURES

source

1. .750  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FG0-bct-n-05-0-UI"  
/tissue\_type="Enchondroma cell line"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP EN1\_2"  
/note="Organ: Bone; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoR I; Site\_2: Not I; NCI CGAP EN1\_2 is a cDNA library containing the following tissue(s): Enchondroma cell line (2 cell lines). The library was constructed according to Bonaldo, Lennon and







[illegible]

25-JUN-1990 (first entry)  
 Human acidic fibroblast growth factor.  
 Acidic fibroblast growth factor.  
 Homo sapiens.  
 EF39773-A.  
 11-JUN-1989.  
 06-JUN-1988; 88EP-0306158.  
 07-JUN-1987; 87US-0070797.  
 (8100) J BIOTECN RES INT.  
 Fiddes JC, Abraham JA, Procter A;  
 WFS, 1989-00876/02.  
 N-250B; AAN2038.  
 Recombinant DNA encoding new fibroblast growth factor  
 containing a mutation that inhibits wound healing and  
 to control neovascularization.  
 Disclousure: Page - 45P; English.  
 See also AAF94038.  
 (Updated on 25-MAR-2003 to correct PA field.)  
 Sequence 155 AA;  
 Query Match 100.0%; Score 825; DN 10; Length 155;  
 Best Local Similarity 100.0%; Pval. No. 3.6e-84;  
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 ABEITTTALTALNPNVYKELVCSNGHFLALPDTVDTESQHTQGL 60  
 2 ABEITTTALTALNPNVYKELVCSNGHFLALPDTVDTESQHTQGL 61  
 61 SASVGVYISTEQVLAHCTGGLVSGTPTRECEFLERENNTYISKAEIN 120  
 62 SASVGVYISTEQVLAHCTGGLVSGTPTRECEFLERENNTYISKAEIN 121  
 121 WFLVGNKSCSGPRTHQKALFLPVSDD 154  
 122 WFLVGNKSCSGPRTHQKALFLPVSDD 155  
 RESULT 7  
 AAF0776 standard; Protein: 155 AA.  
 AAF0776;  
 13-MAY-1986 (first entry)  
 Fibroblast growth factor 1, FGF-1.  
 Conjugate; fibroblast growth factor; FGF; cytokinin; aporin; eye;  
 cell proliferation; regulation; prestyria; corneal clouding; cancer;  
 proinflamm; rheumatoid arthritis.  
 Homo sapiens.  
 W09524921-A2.  
 21-SEP-1995.  
 15-MAR-1995; 95MO-U060448.  
 15-MAR-1994; 94US-021447.  
 15-MAR-1994; 94US-021446.  
 (PRIZ-) PRIZ PHARM INC.  
 Baird JA, Houston LL, Nova MP, Sonowski BA;  
 WPT, 1995-236220/43.  
 New conjugates of growth factor receptor ligand and targeted agent  
 - partic. DNA or cytokinin, used to control cell proliferation in  
 the eye, e.g. to prevent growth of pterygia and corneal clouding  
 Claim 31; Page 140-141; 204P; English.  
 AAF0776-44; are fibroblast growth factors (FGF) FGF-1 to FGF-3  
 used to create an FGF/aporin fusion protein. DNA encoding such fusion  
 proteins are useful for targeting aporin (a cytokinin) to a cell  
 carrying the FGF receptor. Targeted agents (TA) other than aporin  
 include, but are not limited to, retinoids, anti-angiogenic agents,  
 anti-tumor DNA or other cytotoxic agent. The linker sequence within the  
 fusion protein may increase serum stability or intracellular  
 availability of the TA. The conjugates of the invention are used to  
 control cell proliferation in the eye. The conjugates may be used to  
 control cell proliferation in the eye. A specific application is to prevent  
 excessive proliferation of epithelial cells, fibroblasts and  
 cells (for gene therapy). A specific application is to prevent  
 recurrence of pterygia after surgical removal. Closure of  
 trabeculectomy after glaucoma surgery and corneal clouding after  
 ocular laser treatment. Other conditions which may be treated include  
 tumor, cancer, corneal clouding, pterygia, rheumatoid arthritis,  
 complications, Apoptosis, sarcoma and rheumatoid arthritis.  
 Sequence 155 AA;  
 Query Match 100.0%; Score 825; DN 16; Length 155;  
 Best Local Similarity 100.0%; Pval. No. 3.6e-84;  
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 ABEITTTALTALNPNVYKELVCSNGHFLALPDTVDTESQHTQGL 60  
 2 ABEITTTALTALNPNVYKELVCSNGHFLALPDTVDTESQHTQGL 61  
 61 SASVGVYISTEQVLAHCTGGLVSGTPTRECEFLERENNTYISKAEIN 120  
 62 SASVGVYISTEQVLAHCTGGLVSGTPTRECEFLERENNTYISKAEIN 121  
 121 WFLVGNKSCSGPRTHQKALFLPVSDD 154  
 122 WFLVGNKSCSGPRTHQKALFLPVSDD 155  
 RESULT 8  
 AAF75415 standard; Protein: 155 AA.  
 AAF75415;  
 02-MAR-1999 (first entry)  
 Human endothelial cell growth factor precursor protein.  
 Human; endothelial cell growth factor; ECGF; brain stem; probe;  
 hybridisation; bovine; wound healing; prosthetic device.  
 Homo sapiens.  
 Key Location/Qualifiers  
 FT Misc-difference 2.155 /note= "corresponds to beta-ECGF (AAF75414)"  
 FT Misc-difference 16 /note= "sequence of human fibroblast growth factor  
 is homologous to the protein whose sequence  
 starts at this position"  
 FT Misc-difference 22.155 /note= "corresponds to alpha-ECGF (AAF75413)"  
 US527826 A.  
 27-OCT-1998.  
 04-MAY-1996; 96US-0743261.  
 04-MAY-1996; 96US-0743261.  
 29-APR-1995; 95US-0650179.  
 27-MAY-1994; 94US-0738859.  
 03-MAY-1994; 94US-0334884.  
 07-JUN-1995; 95US-0472384.  
 (BROW) BROWN-ROULENC ROGER PHARM INC.

25-JUN-1990 (first entry)  
 Human acidic fibroblast growth factor.  
 Acidic fibroblast growth factor.  
 Homo sapiens.  
 EF39773-A.  
 11-JUN-1989.  
 06-JUN-1988; 88EP-0306158.  
 07-JUN-1987; 87US-0070797.  
 (8100) J BIOTECN RES INT.  
 Fiddes JC, Abraham JA, Procter A;  
 WFS, 1989-00876/02.  
 N-250B; AAN2038.  
 Recombinant DNA encoding new fibroblast growth factor  
 containing a mutation that inhibits wound healing and  
 to control neovascularization.  
 Disclousure: Page - 45P; English.  
 See also AAF94038.  
 (Updated on 25-MAR-2003 to correct PA field.)  
 Sequence 155 AA;  
 Query Match 100.0%; Score 825; DN 10; Length 155;  
 Best Local Similarity 100.0%; Pval. No. 3.6e-84;  
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 ABEITTTALTALNPNVYKELVCSNGHFLALPDTVDTESQHTQGL 60  
 2 ABEITTTALTALNPNVYKELVCSNGHFLALPDTVDTESQHTQGL 61  
 61 SASVGVYISTEQVLAHCTGGLVSGTPTRECEFLERENNTYISKAEIN 120  
 62 SASVGVYISTEQVLAHCTGGLVSGTPTRECEFLERENNTYISKAEIN 121  
 121 WFLVGNKSCSGPRTHQKALFLPVSDD 154  
 122 WFLVGNKSCSGPRTHQKALFLPVSDD 155  
 RESULT 7  
 AAF0776 standard; Protein: 155 AA.  
 AAF0776;  
 13-MAY-1986 (first entry)  
 Fibroblast growth factor 1, FGF-1.  
 Conjugate; fibroblast growth factor; FGF; cytokinin; aporin; eye;  
 cell proliferation; regulation; prestyria; corneal clouding; cancer;  
 proinflamm; rheumatoid arthritis.  
 Homo sapiens.  
 W09524921-A2.  
 21-SEP-1995.  
 15-MAR-1995; 95MO-U060448.  
 15-MAR-1994; 94US-021447.  
 15-MAR-1994; 94US-021446.  
 (PRIZ-) PRIZ PHARM INC.  
 Baird JA, Houston LL, Nova MP, Sonowski BA;  
 WPT, 1995-236220/43.  
 New conjugates of growth factor receptor ligand and targeted agent  
 - partic. DNA or cytokinin, used to control cell proliferation in  
 the eye, e.g. to prevent growth of pterygia and corneal clouding  
 Claim 31; Page 140-141; 204P; English.  
 AAF0776-44; are fibroblast growth factors (FGF) FGF-1 to FGF-3  
 used to create an FGF/aporin fusion protein. DNA encoding such fusion  
 proteins are useful for targeting aporin (a cytokinin) to a cell  
 carrying the FGF receptor. Targeted agents (TA) other than aporin  
 include, but are not limited to, retinoids, anti-angiogenic agents,  
 anti-tumor DNA or other cytotoxic agent. The linker sequence within the  
 fusion protein may increase serum stability or intracellular  
 availability of the TA. The conjugates of the invention are used to  
 control cell proliferation in the eye. The conjugates may be used to  
 control cell proliferation in the eye. A specific application is to prevent  
 excessive proliferation of epithelial cells, fibroblasts and  
 cells (for gene therapy). A specific application is to prevent  
 recurrence of pterygia after surgical removal. Closure of  
 trabeculectomy after glaucoma surgery and corneal clouding after  
 ocular laser treatment. Other conditions which may be treated include  
 tumor, cancer, corneal clouding, pterygia, rheumatoid arthritis,  
 complications, Apoptosis, sarcoma and rheumatoid arthritis.  
 Sequence 155 AA;  
 Query Match 100.0%; Score 825; DN 16; Length 155;  
 Best Local Similarity 100.0%; Pval. No. 3.6e-84;  
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 ABEITTTALTALNPNVYKELVCSNGHFLALPDTVDTESQHTQGL 60  
 2 ABEITTTALTALNPNVYKELVCSNGHFLALPDTVDTESQHTQGL 61  
 61 SASVGVYISTEQVLAHCTGGLVSGTPTRECEFLERENNTYISKAEIN 120  
 62 SASVGVYISTEQVLAHCTGGLVSGTPTRECEFLERENNTYISKAEIN 121  
 121 WFLVGNKSCSGPRTHQKALFLPVSDD 154  
 122 WFLVGNKSCSGPRTHQKALFLPVSDD 155

[illegible]

NY	Burgess W, Drohan MR, Jave M, Maciej TJ;
YI	
IX	WPJ; 1984-564032/56.
XK	PDB#7; AM7571357.
XX	
XX	Compositions for promoting wound healing - containing endothelial:
XX	cell growth factor polypeptides
XX	Example; Fig 8; 23pp; English.
XX	
XX	This sequence represents the complete amino acid sequence of the human
XX	and alpha-ECGF (starting from Ala at position 21; AM751414)
XX	to generate the beta-ECGF (starting from Ala at position 21; AM751414)
XX	the beta-ECGF is cleaved with trypsin, the resulting N-terminal sequence
XX	(a-PHF). The sequence was isolated from a human brain stem cell cDNA
XX	library using a probe designed based on fragments of the bovine ECGF
XX	(see AM751416-475418). The ECGF protein can be used in compositions for
XX	proliferative devices. ECGF is also used to grow cells on a
XX	proliferative device.
XX	
XX	Query Match
XX	Seq Local Similarity 100.0%; Score 825; DB 13; Length 155;
XX	Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	Matche 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	1 ADEGTTTATLTKPNVPPNPKELLYACSGHNPFLPDTQVTVQDQEDHQGL 40
XX	2 ADEGTTTATLTKPNVPPNPKELLYACSGHNPFLPDTQVTVQDQEDHQGL 41
XX	3 SARHGVTPTLTETFGPVNTKPELVLLSYGGSTWPCHEPLLENNVNTYSKQERN 120
XX	42 SARHGVTPTLTETFGPVNTKPELVLLSYGGSTWPCHEPLLENNVNTYSKQERN 121
XX	61 SARHGVTPTLTETFGPVNTKPELVLLSYGGSTWPCHEPLLENNVNTYSKQERN 121
XX	121 MYQLKNSCTSPRPHVTHQGLALPLPVSDD 154
XX	122 MYQLKNSCTSPRPHVTHQGLALPLPVSDD 155
XX	RESULT 10
XX	ID AM75711 standard; Protein; 155 AA.
XX	ID AM75711 standard; Protein; 155 AA.
XX	AM75711;
XX	AM75711;
XX	97-MAR-1998 (direct entry)
XX	Fibroblast growth factor-1.
XX	Fibroblast growth factor-1; PGP-2; murine; protein engineering;
XX	human; fibroblasts; fibroblasts; fibroblasts; fibroblasts;
XX	Human; fibroblasts; fibroblasts; fibroblasts; fibroblasts;
XX	Homo sapiens.
XX	Key Location/Qualifiers
XX	FF FHC difference 100 /note= "The100 is replaced by another amino acid
XX	or Ser"
XX	Gly, Met, Leu or Tyr, especially Ala, Gly
XX	or Ser"
XX	Misc-difference 102 /note= "Glu-102 may be replaced by another amino
XX	acid (Gln10), preferably Ala, Gly or Ser"
XX	/note= "Aan-100 is replaced by another amino
XX	acid (Gln10), preferably Ala, Gly or Ser"
XX	Gly, Met, Leu or Tyr, especially Ala, Gly
XX	or Ser"
XX	Misc-difference 110 /note= "Val-110 may be replaced by another amino
XX	acid (Gln11), preferably Ala, Phe, Ser,
XX	Gly, Met, Leu or Tyr, especially Ala, Gly
XX	or Ser"
XX	N09839436-32.
XX	11-SEP-1998.
XX	01-MAR-1998; 98NO-JPO0078.
XX	01-MAR-1997; 97US-OC040785.
XX	(REDA) EIGAL CO LTD.
XX	Kalyanasaram R, Kawai T, Zhu H;
XX	WPJ; 1998-495843/42.
XX	
XX	This is the amino acid sequence of fibroblast growth factor-1
XX	(PGP-2). Claimed DNA sequences of the invention encode PGP-mucin
XX	polypeptides [see AM75711-20] that show reduced PGP receptor binding
XX	activity but which retain the ability to bind heparin. For PGP-1,
XX	other amino acid residues, with an optional further replacement of
XX	the Glu-102 residue. The mutain may be further modified by
XX	replacement of the Cys residues to reduce aggregation. The mucin
XX	residues are incorporated into a vector and expression
XX	in host cells. The PGP mutants are used to treat heparin-related
XX	disorders, such as excessive bleeding induced by heparin.
XX	Ophthalmic disorders and heparin-associated thrombocytopenia and
XX	thromboses. They may also be used for drug design.
XX	
XX	Sequence 155 AA:
XX	Query Match
XX	Seq Local Similarity 100.0%; Score 825; DB 13; Length 155;
XX	Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	Matche 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





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Query Match      100.0%; Score 425; DB 2; Length 155;
Best local Similarity 100.0%; Pred.No. 3.le-87;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 ABGEITTTTALTEKFLPNPKYKFKLLVCSNGHFLRLIPDTYDTDRSDGNILQL 60

```







ADDRESS: GRAD AND BURNETT LBP  
 STREET, 6305 Columbia Center, 701 Fifth Avenue  
 CITY: Seattle  
 STATE: Washington  
 COUNTRY: USA  
 ZIP: 98104-7092  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 SOFTWARE: PC-DOS/MS-DOS  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patchin Release #1.0, Version #1.15  
 CURRENT APPLICATION DATA: US/09/149 249  
 FILING DATE: 31-MAR-1999  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA: US/09/718,904  
 FILING DATE: 24-SEP-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: No. 650386cbeubing Ph.D., Carol  
 ADDRESS: 650386cbeubing Ph.D., Carol  
 REFERENCE/DOCKET NUMBER: 760190.415C1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4900  
 FAX: (206) 622-4931  
 INFORMATION FOR SEQ ID NO. 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 155 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 FUNCTION:  
 OTHER INFORMATION: /note="POP-1"  
 SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
 PS-09-449-249-10  
 Query Match 100.0%; Score 425; IM 4; Length 155;  
 Best Local Similarity 100.0%; Fwd. No. 3,1a-87;



```

; ABBREVIAT: "Antigenic Glycoprotein"
; TITLE OF INVENTION: PHAGE-DERIVED SUPER PRODUCTION OF
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES
; FILE REFERENCE: PAGE: DATA
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 05/113,288
; PRIORITY DATE: 2000-05-25
; NUMBER OF SEQ. ID NOS: 11
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ. ID NO. 11
; SEQ. ID NO. 15
; SEQ. ID NO. 16
; SEQ. ID NO. 17
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Translated protein sequence for the chemically
; OTHER INFORMATION: synthesized human interferon alpha-2b
US-05-929-911-11

```

[illegible]

```

RESULT 9
US-09-929-945-2
Sequence 2, Application US/0992945
Sequence 1, Application US/0992945
GENERAL INFORMATION
APPLICANT: Stegmann, Thomas
APPLICANT: Kordmann, Vasily A.
APPLICANT: Kordmann, Vasily A.
APPLICANT: Slavchenko, Irina Yu.
APPLICANT: Vozniakov, Oleksandr
TITLE OF INVENTION: SUPER PREDICTION OF RESONANCE
TITLE OF INVENTION: SUPER PREDICTION OF RESONANCE
TITLE OF INVENTION: SUPER PREDICTION OF RESONANCE
FILE REFERENCE: CYBERK-098A
CURRENT APPLICATION NUMBER: US/0992945
CURRENT FILING DATE: 2001-08-15
CURRENT FILING DATE: 2001-08-15
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
SEQ ID NO 135
LOCUS: FASTSEQ
ORGANISM: Homo sapiens

```

[illegible]

```

1  / 1
2  / 2
3  / 3
4  / 4
5  / 5
6  / 6
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[illegible]

RESULT 11  
US-69-J45-373-16  
; Sequence 16, Application US 6934373  
; Publication No. US2001007695A1  
; GENERAL INFORMATION:  
APPLICANT: HUBEN, STEVEN M.  
APPLICANT: JIMENEZ, PABLO  
APPLICANT: DUAN, D. ROXANNE  
APPLICANT: RAMPY, MARK A.  
APPLICANT: KATZMAN, JOHNA  
APPLICANT: RANDOLPH  
APPLICANT: MI, JIAN  
APPLICANT: MOORE, PAUL A.  
APPLICANT: COLEMAN, TIMOTHY A.  
APPLICANT: GILBERT, MICHAEL E.  
APPLICANT: DILLON, PATRICK J.  
APPLICANT: GENIZ, REINER L.  
TITLE OF INVENTION: ERATOINOCYTE FACTOR-2  
NUMBER OF SEQUENCES: 148  
CLASSIFICATION:  
INVENTOR: KESSLER, GOLDSTEIN & FOX, P.L.L.C.  
ADDRESS: 1100 NEW YORK AVENUE, SUITE 690  
STREET:

STATE: DC  
COUNTRY: USA  
ZIP: 26005-3534  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
CONTAINER: 3.5" disk  
COMPUTING SYSTEM: PC/DOS  
SOFTWARE: Patentia 4.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/345,373  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/022,042  
PRIORITY DATE:  
PRIOR APPLICATION DATA:

```

1 FILING DATE: 05-JUN-1995
2 PAK APPLICATION NUMBER: US 60/023,852
3 NAME OF INVENTOR: STEFFE, ERIC K.
4 FILING DATE: 13-AUG-1996
5 PRIOR APPLICATION DATA:
6     ANTIHERPESIN ANTIBODY US 60/031,045
7     FILING DATE: 24-FEB-1997
8 PRIOR APPLICATION DATA:
9     APPLICATION NUMBER: US 68/862,412
10    FILING DATE: 08-SEP-1997
11    APPLICATION NUMBER: US 69/910,975
12    FILING DATE: 13-AUG-1997
13    APPLICATION NUMBER: US 62/055,561
14    FILING DATE: 13-AUG-1997
15    NAME: STEFFE, ERIC K.
16 REGISTRATION NUMBER: 36,418
17 TELEPHONE INFORMATION: 88-036008/RKS
18 TELEPHONE: 202-371-2400
19 TELEFAX: 202-371-2540
20 EMPLOYER: NATIONAL AID
21 SEQUENCE CHARACTERISTICS: 16
22 LENGTH: 135 amino acids
23 ORGANISM: HUMAN
24 STRAIN/DISEASE: No. US2003007455A Relevant
25 TOPOLOGY: No. US2003007455A Relevant
26 MOLECULE TYPE: protein

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	Query Match	100.0%	Score 925	Len: 151	Length 155
	Best Local Similarity	100.0%	Seed No. 4,118-18		
	Matches 151	Conservative	C	Mismatches	0
			Indels	0	Gaps
Qy	1	ABSEITFTTATKNGPFWKPKELLYKNGWGHFAIPDPTVOTGDSRQIQIQ	60		
Dib	2	ABSEITFTTATKNGPFWKPKELLYKNGWGHFAIPDPTVOTGDSRQIQIQ	61		
Qy	61	SANSGWVVIKSTSTGYVANTVGLTGVSTPTCPFLAELENNVNTTSEKAK	120		
Qy	62	SANSGWVVIKSTSTGYVANTVGLTGVSTPTCPFLAELENNVNTTSEKAK	121		
Dib	121	WPKLAKSGKSGWVNTVGLTGVSTPTCPFLAELENNVNTTSEKAK	154		
Dib	122	WPKLAKSGKSGWVNTVGLTGVSTPTCPFLAELENNVNTTSEKAK	155		

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TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE

NUMBER OF SEQUENCES: 128

COUNTRY OF ORIGIN: US

COMPLETION DATE: 01-01-2002

ADDRESS: SEDD AND WESLY LLP

STREET: 6100 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: Washington

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/10/189,360

PRIOR FILING DATE: 02-JUL-2002

CLASSIFICATION: unknown

PRIOR APPLICATION DATA: US/08/718,904

FILING DATE: 31-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: MO; US2003014371AL; eaburg Ph.D., Carol

REFERENCE/DOCKET NUMBER: 760106.415CL

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

FAX: (206) 622-4901

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 155 amino acids

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: peptide

FRAGMENT: YES

OTHER INFORMATION: /note= "PSP-1"

SEQUENCE DESCRIPTION: SEQ ID NO: 10

US-10-189-360-10

Query Match 100.0%; Score 825; DB 12; Length 155;

Best Local Similarity 100.0%; Pseq. No. 4,1e-84;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTTTATTAATKFNPPVKKFLLVCNMGHKLIPDTVFVTSRHTQLGL 60

DB 2 AAGTTTATTAATKFNPPVKKFLLVCNMGHKLIPDTVFVTSRHTQLGL 60

QY 61 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 120

DB 61 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 120

QY 62 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 122

DB 62 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 122

QY 121 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 154

DB 121 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 154

QY 122 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 155

DB 122 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 155

RESULT 13

US-10-081-347-29

Query Match 100.0%; Score 825; DB 12; Length 155;

Best Local Similarity 100.0%; Pseq. No. 4,1e-84;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTTTATTAATKFNPPVKKFLLVCNMGHKLIPDTVFVTSRHTQLGL 60

DB 2 AAGTTTATTAATKFNPPVKKFLLVCNMGHKLIPDTVFVTSRHTQLGL 60

QY 61 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 120

DB 61 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 120

QY 62 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 122

DB 62 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 122

QY 121 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 154

DB 121 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 154

QY 122 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 155

DB 122 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 155

RESULT 14

US-10-280-864-2

Query Match 100.0%; Score 825; DB 12; Length 155;

Best Local Similarity 100.0%; Pseq. No. 4,1e-84;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTTTATTAATKFNPPVKKFLLVCNMGHKLIPDTVFVTSRHTQLGL 60

DB 2 AAGTTTATTAATKFNPPVKKFLLVCNMGHKLIPDTVFVTSRHTQLGL 60

QY 61 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 120

DB 61 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 120

QY 62 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 122

DB 62 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 122

QY 121 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 154

DB 121 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 154

QY 122 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 155

DB 122 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 155

RESULT 15

US-10-280-864-2

Query Match 100.0%; Score 825; DB 12; Length 155;

Best Local Similarity 100.0%; Pseq. No. 4,1e-84;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTTTATTAATKFNPPVKKFLLVCNMGHKLIPDTVFVTSRHTQLGL 60

DB 2 AAGTTTATTAATKFNPPVKKFLLVCNMGHKLIPDTVFVTSRHTQLGL 60

QY 61 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 120

DB 61 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 120

QY 62 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 122

DB 62 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 122

QY 121 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 154

DB 121 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 154

QY 122 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 155

DB 122 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 155

RESULT 16

US-10-280-864-2

Query Match 100.0%; Score 825; DB 12; Length 155;

Best Local Similarity 100.0%; Pseq. No. 4,1e-84;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTTTATTAATKFNPPVKKFLLVCNMGHKLIPDTVFVTSRHTQLGL 60

DB 2 AAGTTTATTAATKFNPPVKKFLLVCNMGHKLIPDTVFVTSRHTQLGL 60

QY 61 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 120

DB 61 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 120

QY 62 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 122

DB 62 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 122

QY 121 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 154

DB 121 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 154

QY 122 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 155

DB 122 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 155

RESULT 17

US-10-280-864-2

Query Match 100.0%; Score 825; DB 12; Length 155;

Best Local Similarity 100.0%; Pseq. No. 4,1e-84;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTTTATTAATKFNPPVKKFLLVCNMGHKLIPDTVFVTSRHTQLGL 60

DB 2 AAGTTTATTAATKFNPPVKKFLLVCNMGHKLIPDTVFVTSRHTQLGL 60

QY 61 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 120

DB 61 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 120

QY 62 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 122

DB 62 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 122

QY 121 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 154

DB 121 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 154

QY 122 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 155

DB 122 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 155

RESULT 18

US-10-280-864-2

Query Match 100.0%; Score 825; DB 12; Length 155;

Best Local Similarity 100.0%; Pseq. No. 4,1e-84;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTTTATTAATKFNPPVKKFLLVCNMGHKLIPDTVFVTSRHTQLGL 60

DB 2 AAGTTTATTAATKFNPPVKKFLLVCNMGHKLIPDTVFVTSRHTQLGL 60

QY 61 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 120

DB 61 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 120

QY 62 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 122

DB 62 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 122

QY 121 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 154

DB 121 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 154

QY 122 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 155

DB 122 MPVGLKNSSCKRPRTVGICALILFLFPVSSD 155

RESULT 19

US-10-280-864-2

Query Match 100.0%; Score 825; DB 12; Length 155;

Best Local Similarity 100.0%; Pseq. No. 4,1e-84;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGTTTATTAATKFNPPVKKFLLVCNMGHKLIPDTVFVTSRHTQLGL 60

DB 2 AAGTTTATTAATKFNPPVKKFLLVCNMGHKLIPDTVFVTSRHTQLGL 60

QY 61 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 120

DB 61 SARGVSVTVTSFTQAAMTGVLGVSOTFNECFPLREPHNTVTSEKAEN 120

QY 6

[illegible]

A;Residues: 1-50 <PAY>

[illegible]

AtMolecule type: protein

[illegible]



[illegible]



[illegible]

[illegible]

## SUMMARY

## ALIGNMENTS

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[illegible]

RP	SEQUENCE FROM N.A.
RQ	SPECIES-Mouse;
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RB	
RC	MEHLING-97128312; PubMed-9572995;
RD	MEHLING-97128312; PubMed-9572995;
RE	"Cloning and characterization of the mouse <i>Zfp-6</i> gene.";
RF	Gen 179-231-238(1996).
RG	[4]
RH	SEQUENCE FROM N.A.
RI	SEQUENCE FROM N.A.
RJ	MEHLING-97094746; PubMed-9519840;
RK	MEHLING-97094746; PubMed-9519840;
RL	Alm K., Frotscher A., Hestermann K.V., Evans J.E., Roeder A.,
RM	Chiu C.M.,
RN	and its expression in the 3B promoter of fibroblast growth factor 1
RO	and its expression in the adult and developing mouse brain."
RP	J. Biol. Chem. 271:30243-30271(1996).
RQ	
RA	-1. FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS
RB	AND INDUCE PROLIFERATION OF CELL TYPES IN
RC	VITRO. THERE ARE DIFFERENCES IN TISSUE DISTRIBUTION AND
RD	CONCENTRATION OF THESE 3 GROWTH FACTORS.
RE	
RF	-1. SUBMITT: Monoclonal.
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[illegible][illegible][illegible]

PA MEDLINE#9076163; PubMed#2849564;  
EX Alencio J., Bailey C., Brou C., Somas T., Courtois M.;  
CY "The expression of the acidic RFP cDNA clone and its  
RT protein product in brain and retina".  
NL FEBS Lett. 242:41-46(1989).  
PM SEQUENCE OF 2-155.  
PM MEDLINE#9019519; PubMed#352197.  
PM MEDLINE#9019519; PubMed#352197.  
EX "Structural evidence that endothelial cell growth factor is the  
precursor of both endothelial cell growth factor alpha and acidic  
endothelial cell growth factor beta".

141	SEQUENCE OF 2-155
EX	MEDLINE#9702586; PubMed#376337;
EN	Crabbe J.M., Krause L.G., Carr S.A., Johnson C.M., Roberts G.D.,
ET	et al. (1996) "The human <i>CD44</i> gene encodes a family of
FT	Complete primary structure of plectin, a rodent epithelial
RT	cell "glue" factor";
RE	(15) Nucleic Acids Res. 24:4988-4993 (1996).
142	SEQUENCE OF 14-155
EX	Medline#9702586; PubMed#470702;
EN	Sequeiros-Gallego G., Rodkey J.P., Bennett C., Rowe-Candoule M.,

RT sequence and homologies." *Proc. Natl. Acad. Sci. USA* 86:3385-3388 (1989).

XX SEQUENCE OF 16-44, AND COMPOSITION.

XX MELLIRME-8605750; PubMed 4085093.

XX MELLIRME-8605750; PubMed 4085093.

XX "Acidic fibroblast growth factor (FGF) from bovine brain: Amino-terminal sequence and comparison with basic FGF." *J. Biol. Chem.* 264: 4129-4134 (1989).

XX "Acidic fibroblast growth factor (FGF) from bovine brain: Amino-terminal sequence and comparison with basic FGF." *J. Biol. Chem.* 264: 4129-4134 (1989).

XX SEQUENCE OF 16-56 FROM N.A. SECT.

XX SEQUENCE OF 16-56 FROM N.A. SECT.

Myers R.A., Gopodrowicz D., Fiddes J.C.,  
"Nucleotide sequence of a bovine clone encoding the angiogenic

[illegible]

[illegible]









50	SEQUENCE	156 AA; 22103 MW; D6R6447377E6043 CXC64;	45.0%; Source 404.5; DM 4; Length 136;
	Query Match		
	Local similarity	32.6%; Pred. No. 6.4e-31;	
	Machine #41	Conservative 45; Miscellaneous 51; Indels 5; Gaps 2;	
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0y	65	ASGHTTALTEFN--LPQWKKFLKCYHMGHAFILPQVOTVDESDHQ 57	

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GENERAL INFORMATION:
  APPLICANT: Stegmann, Thomas
  APPLICANT: Rodymov, Vitaliy A.
  APPLICANT: Savelchenko, Evgen Yu.
  APPLICANT: Savelchenko, Evgen Yu.
  APPLICANT: Vozniakov, Oleksandr
  TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
  TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
  TITLE OF INVENTION: SUPER PRODUCTION OF RECOMBINANT
  FILE REFERENCE: CUBEN-008A
  FILE REFERENCE: CUBEN-008A
  CURRENT APPLICATION NUMBER: US/09/924,945
  CURRENT FILING DATE: 2001-08-15
  CURRENT FILING DATE: 2001-08-15
  CURRENT FILING DATE: 2001-08-15
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[illegible]

STREET: One Cynamid Plaza  
CITY: Fort Wayne  
STATE: Indiana  
COUNTRY: United States  
ZIP: 46740-4426  
COMPUTER READABLE FORM:  
CHARACTER SET: 1144 mb diacritic  
COMPUTER: IBM PC  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Word Processor  
FILE NAME: 1144 mb diacritic  
APPLICATION NUMBER: US/98/296.3739  
FILING DATE: August 15, 1994  
PREVIOUS APPLICATION NUMBER:  
FILING DATE: 09/126.973  
ATTORNEY/AGENT INFORMATION:  
FIRM: The Law Firm of  
REGISTRATION NUMBER: 14088  
REFERENCE/DOCKET NUMBER: 854-908CIP 132.063)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 317-432-1342  
TELEFAX: 317-432-1305  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30  
TYPE: chemical  
FEATURES:  
TOPOLOGY: single  
STRANDNESS: single  
NOISE: linear  
DESCRIPTION: DNA encoding a protein  
SEQUENCE TYPE: entire sequence  
SEQUENCE SOURCE: constructed  
FEATURES:  
OTHER INFORMATION: SEQ-7 having surface loop  
OTHER INFORMATION: residues 116 to 122 replaced with corresponding  
OTHER INFORMATION: structural elements from borvis FGF-1  
US-01-290-3739-16

[illegible]



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: CURRENT APPLICATION NUMBER: US/09/529,916
:
: CURRENT FILING DATE: 2001-08-15
: PRIOR APPLICATION NUMBER: 09/318,288
: PRIOR FILING DATE: 1999-05-25
:
: NUMBER OF SEQ ID NOS: 11
: SOFTWARE: FASTSEQ for Windows Version 4.0
:
: SEQ ID NO 3
: LENGTH: 468
: TYPE: DNA
: ORGANISM: Homo sapiens

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Alignment Scores:

Prod. No.	1,226-107	Length	468
Score	825.00	Matches	154
Percent Similarity	100.00%	Conservative	0
Best Local Similarity	100.00%	Mismatches	0
Query Match	100.00%	Indels	0
DB:	5	Gaps	0

US-010-022-554A-4 (1-158) X US-09-939-918-3 (2-468)

[illegible][illegible][illegible]

US 95-929-946-3  
: Sequence 3, Application US/69929945  
: Patent No. US2002015552A2  
: GENERAL INFORMATION  
: APPLICANT: Stegmann, Thomas  
: APPLICANT: Stegmann, Thomas  
: APPLICANT: Stegmann, Thomas  
: APPLICANT: Cherkovsk, Svetlana A.  
: APPLICANT: Slavchenko, Irina Yu.  
: APPLICANT: Voronov, Olexander

```

1 FILE REFERENCE: C:\WINDOWS\LOGON.SCR
2
3 CURRENT APPLICATION NUMBER: US/99/925,945
4
5 CURRENT FILING DATE: 2001-06-15
6
7 NUMBER OF SEQ ID NOS: 8
8
9 SOFTWARE: FASTSEQ for Windows Version 4.0
10
11 SEQ ID NO: 1
12 LENGTH: 145
13
14 TYPE: DNA
15
16 ORGANISM: Homo sapiens

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Alignment Scores:		
Fred No.:	1,226-107	468
Length:		
Matches:	925.0	154
Score:	100.00%	
Percent Similarity:	100.00%	Conservative: 0
Local Similarity:	100.00%	Minimales: 0
Query Match:	100.00%	Indels: 0
Gaps:	0	0

[illegible]

GENERAL INFORMATION:  
 APPLICANT: Seegans, Thomas  
 APPLICANT: Seegans, Vitalis A.  
 APPLICANT: Carstoph, Swilens I.  
 APPLICANT: Slivchenko, Iryna Yu.  
 APPLICANT: Voroshov, Olexander  
 TITLE OF INVENTION: SUPER MODIFICATION OF RECOMBINANT  
 TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR 155  
 FILE REFERENCE: OVINGR.009A  
 CURRENT APPLICATION NUMBER: US/10/649,480

PRIOR APPLICATION NUMBER: 207069, SMC  
 PRIOR FILING DATE: 2003-03-27  
 NUMBER OF SEQ ID NOS: 8  
 SOFTWARE: FASTSEQ for Windows Version 4.0  
 SEQ ID NO 3  
 LENGTH: 468  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 IS-10-(449-480-3)

1. 15	Length:	1.224-1.07
1. 15	Matches:	825.00
1. 15	Conservative:	100.00%
1. 15	Mismatches:	100.00%
1. 15	Indels:	100.00%
1. 15	Gaps:	17

Accession	Gene	Accession	Gene
21	hAcrTyr12y1y2y3y4y5y6y7y8y9y10y11y12y13y14y15y16y17y18y19y20y21y22y23y24y25y26y27y28y29y30y31y32y33y34y35y36y37y38y39y40y41y42y43y44y45y46y47y48y49y50y51y52y53y54y55y56y57y58y59y60y61y62y63y64y65y66y67y68y69y70y71y72y73y74y75y76y77y78y79y80y81y82y83y84y85y86y87y88y89y90y91y92y93y94y95y96y97y98y99y100y101y102y103y104y105y106y107y108y109y110y111y112y113y114y115y116y117y118y119y120y121y122y123y124y125y126y127y128y129y130y131y132y133y134y135y136y137y138y139y140y141y142y143y144y145y146y147y148y149y150y151y152y153y154y155y156y157y158y159y160y161y162y163y164y165y166y167y168y169y170y171y172y173y174y175y176y177y178y179y180y181y182y183y184y185y186y187y188y189y190y191y192y193y194y195y196y197y198y199y200y201y202y203y204y205y206y207y208y209y210y211y212y213y214y215y216y217y218y219y220y221y222y223y224y225y226y227y228y229y230y231y232y233y234y235y236y237y238y239y240y241y242y243y244y245y246y247y248y249y250y251y252y253y254y255y256y257y258y259y260y261y262y263y264y265y266y267y268y269y270y271y272y273y274y275y276y277y278y279y280y281y282y283y284y285y286y287y288y289y290y291y292y293y294y295y296y297y298y299y300y301y302y303y304y305y306y307y308y309y310y311y312y313y314y315y316y317y318y319y320y321y322y323y324y325y326y327y328y329y330y331y332y333y334y335y336y337y338y339y340y341y342y343y344y345y346y347y348y349y350y351y352y353y354y355y356y357y358y359y360y361y362y363y364y365y366y367y368y369y370y371y372y373y374y375y376y377y378y379y380y381y382y383y384y385y386y387y388y389y390y391y392y393y394y395y396y397y398y399y400y401y402y403y404y405y406y407y408y409y410y411y412y413y414y415y416y417y418y419y420y421y422y423y424y425y426y427y428y429y430y431y432y433y434y435y436y437y438y439y440y441y442y443y444y445y446y447y448y449y450y451y452y453y454y455y456y457y458y459y460y461y462y463y464y465y466y467y468y469y470y471y472y473y474y475y476y477y478y479y480y481y482y483y484y485y486y487y488y489y490y491y492y493y494y495y496y497y498y499y500y501y502y503y504y505y506y507y508y509y510y511y512y513y514y515y516y517y518y519y520y521y522y523y524y525y526y527y528y529y530y531y532y533y534y535y536y537y538y539y540y541y542y543y544y545y546y547y548y549y550y551y552y553y554y555y556y557y558y559y560y561y562y563y564y565y566y567y568y569y570y571y572y573y574y575y576y577y578y579y580y581y582y583y584y585y586y587y588y589y590y591y592y593y594y595y596y597y598y599y600y601y602y603y604y605y606y607y608y609y610y611y612y613y614y615y616y617y618y619y620y621y622y623y624y625y626y627y628y629y630y631y632y633y634y635y636y637y638y639y640y641y642y643y644y645y646y647y648y649y650y651y652y653y654y655y656y657y658y659y660y661y662y663y664y665y666y667y668y669y670y671y672y673y674y675y676y677y678y679y680y681y682y683y684y685y686y687y688y689y690y691y692y693y694y695y696y697y698y699y700y701y702y703y704y705y706y707y708y709y710y711y712y713y714y715y716y717y718y719y720y721y722y723y724y725y726y727y728y729y730y731y732y733y734y735y736y737y738y739y740y741y742y743y744y745y746y747y748y749y750y751y752y753y754y755y756y757y758y759y760y761y762y763y764y765y766y767y768y769y770y771y772y773y774y775y776y777y778y779y780y781y782y783y784y785y786y787y788y789y790y791y792y793y794y795y796y797y798y799y800y801y802y803y804y805y806y807y808y809y810y811y812y813y814y815y816y817y818y819y820y821y822y823y824y825y826y827y828y829y830y831y832y833y834y835y836y837y838y839y840y841y842y843y844y845y846y847y848y849y850y851y852y853y854y855y856y857y858y859y860y861y862y863y864y865y866y867y868y869y870y871y872y873y874y875y876y877y878y879y880y881y882y883y884y885y886y887y888y889y890y891y892y893y894y895y896y897y898y899y900y901y902y903y904y905y906y907y908y909y910y911y912y913y914y915y916y917y918y919y920y921y922y923y924y925y926y927y928y929y930y931y932y933y934y935y936y937y938y939y940y941y942y943y944y945y946y947y948y949y950y951y952y953y954y955y956y957y958y959y960y961y962y963y964y965y966y967y968y969y970y971y972y973y974y975y976y977y978y979y980y981y982y983y984y985y986y987y988y989y990y991y992y993y994y995y996y997y998y999y1000y1001y1002y1003y1004y1005y1006y1007y1008y1009y1010y1011y1012y1013y1014y1015y1016y1017y1018y1019y1020y1021y1022y1023y1024y1025y1026		

184	AQTGCGGAAAGCGTGTGGGAGGGGTGTTATATAAAGATACCGAG	bb
81	WetApTh2ApGlyLeuLeuGlyGlySerGlnThrProGln	yy
344	ATGGACACACACCGCGCTTTTATTCGGCTACACGACGCCGAA	bb
101	GluArgLeuGluGluAsnGlyThrMetThrTyrLeuSerLeu	yy

121	TzppheGvGlyVzsdvzGzshakgQlYseCvdyahgQl	yy
364	TQgTzTtTtTtTtTtTtTtTtTtTtTtTtTtTtTtTt	zb
141	GLSLyallZLefepheGvProGvProValSeSeZstap	yy
424	CAGMAAGCACTCTTCTTCTTCTTCTTCTTCTTCTT	zb

RESULT 5

PUBLICATION NO. US2003015746A1  
PRIORITY OF JP2002-098700 IS CLAIMED.  
GENERAL INFORMATION:  
APPLICANT: NANA, HIROYUKI  
APPLICANT: TAKAHASHI, HITOSHI  
APPLICANT: IRTANI, SHUJI  
TITLE OF INVENTION: METHOD FOR DIAGNOSING SCHIZOPHRENIA  
FILE REFERENCE: 2154479US/CONC  
CURRENT APPLICATION NUMBER: US10/388,410  
CURRENT FILING DATE: 2003-03-17

PRIOR FILING DATE: 2000-11-28  
 PRIOR APPLICATION NUMBER: JP 2000-061775  
 PRIOR FILING DATE: 2000-01-07  
 NUMBER OF SEQ ID NOS: 10  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 8  
 LENGTH: 490  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-168-410-8

Length:	1.3e-107	45
Matches:	\$25.00	15
Conservative:	100.00%	0
Mismatches:	100.00%	0
Indels:	100.00%	0
Gaps:	15	0
Alignment Scores:		
Prod. No.:		
Score:		
Percent Similarity:		
Percent Local Similarity:		
Query Match:		
DB:		

[illegible]

1 PRIOR FILING DATE: 2001-08-15  
2 NUMBER OF SEQ ID NOS: 8  
3 SOFTWARE: FASTSEQ for Windows Version 4.0  
4 SEQ ID NO: 1  
5 LENGTH: 610  
6 TYPE: DNA  
7 ORGANISM: Artificial Sequence  
8 OTHER INFORMATION: Chemically synthesized sequence for human acidic  
9 OTHER INFORMATION: Fibroblast Growth Factor (155 amino acids) using  
10 OTHER INFORMATION: Preferred codons for E. coli  
11 NAME/KEY: CDS  
12 LOCATION: (122)...(599)  
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[illegible]



**CNA Library Arrayed by:** Greg Lennon, Ph.D.  
**DNA Sequencing by:** Washington University Genomic Sequencing Center  
**Genetic Mapping Information can be found through the I.M.A.G.E. Consortium at:**  
[www-bio.lnll.gov/hbp/wasg/image.html](http://www-bio.lnll.gov/hbp/wasg/image.html)  
**Accession Number:** U08697  
**Size:** 384 spots per array  
**High quality sequence stop:** 45%  
**Location/Qualifiers:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	No.	Result	Query	Score	Length	ID	Description
c	1	825	100.0	821	12	B1528900	A
	2	825	100.0	821	12	B1528900	A1529150 603250534
	3	825	100.0	1014	12	BME09005	BME09005 AGNCOUNT
	4	825	100.0	1014	12	BME09005	BME09005 AGNCOUNT
	5	825	100.0	1014	12	BME09005	BME09005 AGNCOUNT
	6	825	100.0	1014	12	BME09005	BME09005 AGNCOUNT
	7	790	95.9	878	12	B1753445	B1753445 603027256
	8	790	95.9	878	12	B1753445	B1753445 603027256
	9	790	95.9	878	12	B1753445	B1753445 603027256
	10	790	95.9	878	12	B1753445	B1753445 603027256
c	11	784	95.2	832	12	B1659731	B1659731 603294333
	12	784	95.2	832	12	B1659731	B1659731 603294333
	13	784	95.2	832	12	B1659731	B1659731 603294333
	14	784	95.2	832	12	B1659731	B1659731 603294333
	15	784	95.2	832	12	B1659731	B1659731 603294333
	16	784	95.2	832	12	B1659731	B1659731 603294333
	17	784	95.2	832	12	B1659731	B1659731 603294333
	18	784	95.2	832	12	B1659731	B1659731 603294333
	19	784	95.2	832	12	B1659731	B1659731 603294333
	20	784	95.2	832	12	B1659731	B1659731 603294333
c	21	757.5	91.8	2206	13	B1629233	B1629233 603277577
	22	757.5	91.8	2206	13	B1629233	B1629233 603277577
	23	757.5	91.8	2206	13	B1629233	B1629233 603277577
	24	757.5	91.8	2206	13	B1629233	B1629233 603277577
	25	757.5	91.8	2206	13	B1629233	B1629233 603277577
	26	757.5	91.8	2206	13	B1629233	B1629233 603277577
	27	757.5	91.8	2206	13	B1629233	B1629233 603277577
	28	757.5	91.8	2206	13	B1629233	B1629233 603277577
	29	757.5	91.8	2206	13	B1629233	B1629233 603277577
	30	757.5	91.8	2206	13	B1629233	B1629233 603277577
c	31	695	73.5	621	13	B1840137	B1840137 602073431
	32	695	73.5	621	13	B1840137	B1840137 602073431
	33	695	73.5	621	13	B1840137	B1840137 602073431
	34	695	73.5	621	13	B1840137	B1840137 602073431
	35	695	73.5	621	13	B1840137	B1840137 602073431
	36	695	73.5	621	13	B1840137	B1840137 602073431
	37	695	73.5	621	13	B1840137	B1840137 602073431
	38	695	73.5	621	13	B1840137	B1840137 602073431
	39	695	73.5	621	13	B1840137	B1840137 602073431
	40	695	73.5	621	13	B1840137	B1840137 602073431
c	41	596	72.2	443	9	A1632100	A1632100 602714321
	42	596	72.2	443	9	A1632100	A1632100 602714321
	43	596	72.2	443	9	A1632100	A1632100 602714321
	44	596	72.2	443	9	A1632100	A1632100 602714321
	45	596	72.2	443	9	A1632100	A1632100 602714321
	46	596	72.2	443	9	A1632100	A1632100 602714321
	47	596	72.2	443	9	A1632100	A1632100 602714321
	48	596	72.2	443	9	A1632100	A1632100 602714321
	49	596	72.2	443	9	A1632100	A1632100 602714321
	50	596	72.2	443	9	A1632100	A1632100 602714321
c	51	585	69.0	385	14	C0574341	C0574341 603260700
	52	585	69.0	385	14	C0574341	C0574341 603260700
	53	585	69.0	385	14	C0574341	C0574341 603260700
	54	585	69.0	385	14	C0574341	C0574341 603260700
	55	585	69.0	385	14	C0574341	C0574341 603260700
	56	585	69.0	385	14	C0574341	C0574341 603260700
	57	585	69.0	385	14	C0574341	C0574341 603260700
	58	585	69.0	385	14	C0574341	C0574341 603260700
	59	585	69.0	385	14	C0574341	C0574341 603260700
	60	585	69.0	385	14	C0574341	C0574341 603260700
c	61	562.5	68.2	364	9	A1644448	A1644448 W35007.X
	62	562.5	68.2	364	9	A1644448	A1644448 W35007.X
	63	562.5	68.2	364	9	A1644448	A1644448 W35007.X
	64	562.5	68.2	364	9	A1644448	A1644448 W35007.X
	65	562.5	68.2	364	9	A1644448	A1644448 W35007.X
	66	562.5	68.2	364	9	A1644448	A1644448 W35007.X
	67	562.5	68.2	364	9	A1644448	A1644448 W35007.X
	68	562.5	68.2	364	9	A1644448	A1644448 W35007.X
	69	562.5	68.2	364	9	A1644448	A1644448 W35007.X
	70	562.5	68.2	364	9	A1644448	A1644448 W35007.X
c	71	548	66.6	334	10	B1624255	B1624255 603277016
	72	548	66.6	334	10	B1624255	B1624255 603277016
	73	548	66.6	334	10	B1624255	B1624255 603277016
	74	548	66.6	334	10	B1624255	B1624255 603277016
	75	548	66.6	334	10	B1624255	B1624255 603277016
	76	548	66.6	334	10	B1624255	B1624255 603277016
	77	548	66.6	334	10	B1624255	B1624255 603277016
	78	548	66.6	334	10	B1624255	B1624255 603277016
	79	548	66.6	334	10	B1624255	B1624255 603277016
	80	548	66.6	334	10	B1624255	B1624255 603277016
c	81	534	65.8	398	14	C1024140	C1024140 AGNCOUNT
	82	534	65.8	398	14	C1024140	C1024140 AGNCOUNT
	83	534	65.8	398	14	C1024140	C1024140 AGNCOUNT
	84	534	65.8	398	14	C1024140	C1024140 AGNCOUNT
	85	534	65.8	398	14	C1024140	C1024140 AGNCOUNT
	86	534	65.8	398	14	C1024140	C1024140 AGNCOUNT
	87	534	65.8	398	14	C1024140	C1024140 AGNCOUNT
	88	534	65.8	398	14	C1024140	C1024140 AGNCOUNT
	89	534	65.8	398	14	C1024140	C1024140 AGNCOUNT
	90	534	65.8	398	14	C1024140	C1024140 AGNCOUNT
c	91	524	63.4	642	10	B0670495	B0670495 60321431
	92	524	63.4	642	10	B0670495	B0670495 60321431
	93	524	63.4	642	10	B0670495	B0670495 60321431
	94	524	63.4	642	10	B0670495	B0670495 60321431
	95	524	63.4	642	10	B0670495	B0670495 60321431
	96	524	63.4	642	10	B0670495	B0670495 60321431
	97	505	63.2	522	14	C0201495	C0201495 603200090
	98	505	63.2	522	14	C0201495	C0201495 603200090
	99	505	63.2	522	14	C0201495	C0201495 603200090
	100	505	63.2	522	14	C0201495	C0201495 603200090
c	101	476.5	57.8	701	12	B9952510	B9952510 U-I-EDD-
	102	476.5	57.8	701	12	B9952510	B9952510 U-I-EDD-
	103	476.5	57.8	701	12	B9952510	B9952510 U-I-EDD-
	104	476.5	57.8	701	12	B9952510	B9952510 U-I-EDD-
	105	476.5	57.8	701	12	B9952510	B9952510 U-I-EDD-
	106	476.5	57.8	701	12	B9952510	B9952510 U-I-EDD-
	107	476.5	57.8	701	12	B9952510	B9952510 U-I-EDD-
	108	476.5	57.8	701	12	B9952510	B9952510 U-I-EDD-
	109	476.5	57.8	701	12	B9952510	B9952510 U-I-EDD-
	110	476.5	57.8	701	12	B9952510	B9952510 U-I-EDD-
c	111	447	54.2	336	10	B8850804	B8850804 603277278
	112	447	54.2	336	10	B8850804	B8850804 603277278
	113	447	54.2	336	10	B8850804	B8850804 603277278
	114	447	54.2	336	10	B8850804	B8850804 603277278
	115	447	54.2	336	10	B8850804	B8850804 603277278
	116	447	54.2	336	10	B8850804	B8850804 603277278
	117	447	54.2	336	10	B8850804	B8850804 603277278
	118	447	54.2	336	10	B8850804	B8850804 603277278
	119	447	54.2	336	10	B8850804	B8850804 603277278
	120	447	54.2	336	10	B8850804	B8850804 603277278
c	121	447	54.2	336	10	B8850804	B8850804 603277278
	122	447	54.2	336	10	B8850804	B8850804 603277278
	123	447	54.2	336	10	B8850804	B8850804 603277278
	124	447	54.2	336	10	B8850804	B8850804 603277278
	125	447	54.2	336	10	B8850804	B8850804 603277278
	126	447	54.2	336	10	B8850804	B8850804 603277278
	127	447	54.2	336	10	B8850804	B8850804 603277278
	128	447	54.2	336	10	B8850804	B8850804 603277278
	129	447	54.2	336	10	B8850804	B8850804 603277278
	130	447	54.2	336	10	B8850804	B8850804 603277278

Y Y C I N D I T I S 1 0 6 0

RESULT 1	514 bp	WGA	linear	A1590078		
LOCUS	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
REFERENCE	1	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999
ACCESSION	U00001	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999
DEFINITION	U00001	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999
ORGANISM	U00001	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999
FEATURES	U00001	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999
ORIGIN	U00001	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999
COMMENTS	U00001	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999
DESCRIPTION	U00001	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999
KEYWORDS	U00001	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999
REFERENCES	U00001	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999
1	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
2	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
3	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
4	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
5	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
6	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
7	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
8	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
9	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
10	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
11	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
12	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
13	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
14	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
15	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
16	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
17	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
18	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
19	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
20	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
21	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
22	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
23	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
24	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
25	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
26	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
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31	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
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33	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
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44	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
45	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
46	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
47	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	
48	NCI_CGAP_Hm25	mouse	spine	chima	EST 21-APR-1999	

found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLNL11764 row: k column: 23  
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## FEATURES

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poly(A) mRNA fragments by  
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position: 10% poly(A)  
[NMH/MNMT, Metabolic Insec-  
tion]; A NIH MOC Library."
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ORIGIN

**ORIGIN**

[illegible]

RESULT 3  
BM809005

[illegible]

FEATURES



[illegible]

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